

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:10:39 ; Search time 549,862 Seconds
(without alignments)
2453.577 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700

Sequence: 1 QVQLQSGAELKPGESLKI...AKWPEYFQHWGQGLVTVSS 129

Scoring table

BLOSUM62			
Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum

Listing first 45 summaries

```

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-O=/abs/ABSSWEE pool/ustp092640/runat.25052006.15711.5825/app_query.fasta_1
-DB=n_GeneSeq -OEM=fastp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits START=1 -END=1 -MATRIX=dlbsummed -TRANS=human4.0.cdi -LIST=45
DOCLALIGN=200 -THR_SCORE=500 -THR_MAX=100 -THR_MIN=0 -ALIGN=5 -MODE=LOCAL
-OUTFMT=ptc -NORM=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05sh
-USER=ust092640@CGN_1_1.942.@runat.25052006.15711.5825 -NCPU=6 -ICPU=3
-NO_MMAP -NSG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEB_TEMPL=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAOP=10 -XGAPEXT=0.5 -FGAOP=6 -FGAPEXT=7
-XGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

```
Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn190s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	700	100.0	765	6	AAD32664	Aad32664 Chimeric
2	697	99.6	774	2	AAI50787	C6 human
3	694	99.1	807	6	AAD32665	Aad32665 Chimeric

4	694	99.1	846	6	AAD32666	AAD32666 Chimeric
5	694	99.1	861	6	AAD32667	AAD32667 Chimeric
6	694	99.1	873	6	AAD32669	AAD32669 Chimeric
7	694	99.1	887	6	AAD32668	AAD32668 Chimeric
8	629	89.9	387	4	AAS03465	AAS03465 DNA encod
9	540	77.1	364	15	AEEO3776	AEEO3776 Anticbody
10	540	77.1	306	5	AAFe61513	AAFe61513 DNA encod
11	539	77.0	369	14	AEBO1074	AEBO1074 Human IPT
12	534.5	76.4	660	10	ABZ74803	ABZ74803 Human ant
13	532.5	76.1	666	10	ABZ74798	ABZ74798 Human ant
14	532.5	76.1	666	10	ABZ74810	ABZ74810 Human ant
15	532.5	76.1	672	10	ABZ74813	ABZ74813 Human ant
16	531	75.9	669	10	ABZ74791	ABZ74791 Human ant
17	530.5	75.8	379	10	ADK18645	ADK18645 Anti-huma
18	530.5	75.8	379	12	ADL25432	ADL25432 Human mAb
19	529	75.6	669	10	ABZ74812	ABZ74812 Human ant
20	528.5	75.5	379	10	ADK18653	ADK18653 Anti-huma
21	528.5	75.5	379	10	ADK18641	ADK18641 Anti-huma
22	528.5	75.5	379	12	ADL25439	ADL25439 Human mAb
23	528.5	75.5	379	12	ADL25415	ADL25415 Human mAb
24	528.5	75.5	666	10	ABZ74804	ABZ74804 Human ant
25	528	75.4	730	3	AAZ29000	AAZ29000 Anti-mur
26	527.5	75.4	438	4	AAH41155	AAH41155 Human cod
27	527	75.3	351	6	AAI43585	AAI43585 Digi anti
28	527	75.3	351	8	ACC47587	ACC47587 Human ant
29	526.5	75.2	666	10	ABZ74799	ABZ74799 Human ant
30	526.5	75.2	672	10	ABZ74793	ABZ74793 Human ant
31	526	75.1	369	13	ADS15292	ADS15292 Heavy cha
32	526	75.1	669	10	ABZ74800	ABZ74800 Human ant
33	525	75.0	669	10	ABZ74807	ABZ74807 Human ant
34	524	74.9	357	10	ADD69255	ADD69255 Human ant
35	523.5	74.8	379	10	ADK18664	ADK18664 Anti-huma
36	523.5	74.8	379	12	ADL25459	ADL25459 Human mAb
37	523.5	74.8	666	10	ABZ74816	ABZ74816 Human ant
38	523.5	74.8	732	6	ABSS5608	ABSS5608 DNA encod
39	520	74.3	462	2	AAT73442	AAT73442 Human imm
40	520	74.3	462	2	AAV39240	AAV39240 Functiona
41	520	74.3	462	2	AAZ21594	AAZ21594 Particl n
42	519	74.1	351	15	AEFZ4185	AEFZ4185 Human INF
43	519	74.1	351	15	AEFZ4186	AEFZ4186 Human INF
44	519	74.1	469	8	AAO56222	AAO56222 Human AB-
45	519	74.1	469	14	AEAI6228	AEAI6228 Anti-huma

ALIGNMENTS

RESULT 1	
AAD32664	
ID	AAD32664 standard; DNA; 765 BP.

XX	29-AUG-2003	(revised)
DT	18-JUN-2002	(first entry)
DT		

DE Chimeric SCBP C6.5 SFV DNA

KM Gene-delivery compound; single-chain binding polypeptide; SCBP; gene,
KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.

OS	Homo sapiens.
OS	Mus sp.
OS	Chimeric.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

XX 03-JAN-2002.
 PD 25-JUN-2001; 2001WO-US020182.
 XX 23-JUN-2000; 2000US-0213653P.
 XX (HUST/) HUSTON J S.
 PA (WILS/) WILS P.
 PA (QUAN/) QUAN Z.
 PA (LAUR/) LAURENT O.
 PA (MARA/) MARASCO W A.
 PA (SCHE/) SCHERMAN D.
 XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
 PI WPI; 2002-268789/31.
 DR P-PSDB; AAE20407.
 XX
 XX Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associated moiety coupled to polypeptide by
 FT residue.
 FT
 XX
 PS Disclosure: Fig 4; 96pp; English.
 XX
 XX The invention relates to gene-delivery compound comprising a single-chain
 CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6.5 afv DNA
 CC comprising human and murine sequences. (updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 765 BP; 155 A; 217 C; 227 G; 166 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,31e-64 Length: 765
 Score: 700.00 Matches: 129
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-092-640-32 (1-129) x AAD32664 (1-765)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
 DB 1 CAGGTCACTGTTGCAAGTCTGGGCGAGATTGAAAAACCGGGGAGTCTCGAAGATC 60
 QY 21 SerCySlyGlyGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgMet 40
 DB 61 TCCCTGAAAGGTTCTGATACAGCTTACCAGCTGATCCCTCGGGGCGCCGCAAGT 120
 QY 41 ProGlyLysGlyLeuGlnLysTyrMetGlyLeuIleTyrProGlyLysPheSerThrLysTyr 60
 DB 121 CCCGGGAAAGGCTTGAGATCAATGGGGCTCATATATCTCGGTGACTCTGACACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 181 AGCCGCTCTCCAAAGCCAGGCAAGTCACTGCTGACAGATCCGTCAGCACTGCTAC 240
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
 DB 241 TTGCAATGAGCAGTCTGGAAGCCCTCGACAGCGCGTGAATTTTGTGCGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerAsnCysAlaValTyrProGlyLysPheGlnHisTyrGly 120
 DB 301 GGGGATATTGCGATGTTCCAACTGCGCAAGTGGCGTGAATTAATTCCAGCATTTGGGGC 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129

DB 361 CAGGGACCCCTGTCACGCTCTCTCA 387

RESULT 2

AAT50787
 ID AAT50787 standard; DNA; 774 BP.

AC AAT50787;

DT 23-SEP-1997 (first entry)

DE C6 human sFv antibody C6.5 encoding DNA.

KW Tumour; immune response; cytotoxin; carcinoma; breast cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..774

FT /tag= a

FT /product= "Antibody C6.5"

FT /transl_except= (pos: 181..183, aa: Ser)

FT /transl_except= (pos: 361..363, aa: Gly)

FT /transl_except= (pos: 421..423, aa: Gly)

FT /note= "Without stop codon"

XX MO9700271-A1.

XX 03-JAN-1997.

XX 13-JUN-1996; 96WO-US010287.

XX 14-JUN-1995; 95US-0000238P.

XX 15-JUN-1995; 95US-0000250P.

XX (REGC) UNIV CALIFORNIA.

XX Marke JD, Schier R;

XX WPI; 1997-077488/07.

XX P-PSDB; AAM08487.

XX New C6 human antibody binding specifically to c-erbB-2 - useful for

XX treatment and diagnosis of tumours, with reduced risk of generating

XX immune response.

XX Claim 4; Fig 1; 117pp; English.

XX The present sequence encodes a C6 human antibody C6.5, that binds

XX specifically to c-erbB-2. A chimeric molecule that binds specifically to

XX tumour cells carrying c-erbB-2 consists of an effector compound attached

XX to a C6 human antibody, e.g. C6.5. If the effector compound is a

XX cytotoxin the chimeric molecule can be used to inhibit growth of c-erbB-2

XX positive tumours (especially breast and other carcinomas). If the

XX effector compound is a label the chimeric molecule can be used to detect

XX such cells, including in vivo localisation. The antibody can also be used

XX for diagnosis/localisation, in vivo or in vitro, especially by

XX immunassay. The nucleic acid encoding the antibody, and a nucleic acid

XX encoding a single chain polypeptide with the binding specificity of the

XX antibody and comprising the binding portions of variable regions of light

XX and heavy chains of the antibody, joined by a linker, can be used to

XX produce recombinant proteins by standard methods. Unlike known anti-c-

XX erbB-2 antibodies, C6 antibodies are fully human, so should elicit

XX little, if any, immunogenic response

SQ Sequence 774 BP; 156 A; 222 C; 230 G; 166 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,05e-64 Length: 774
 Score: 697.00 Matches: 128
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 99.2% Mismatches: 0
 Query Match: 99.6% Indels: 0
 DB: Gaps: 0

US-10-092-640-32 (1-129) x AAT50787 (1-774)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLeuLysProGlyGlnSerLeuLysIle 20
 Db 1 CAGGTCACTGTTGACAGTCTGGGGCAGAGTTGAAAAAACCAGGAGTCTCGAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 Db 61 TCCTGTAAGGGTTCGTGATACACCTTACACGCTTACCTGAGTCCCTGGGCGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGlnLysTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
 Db 121 CCGGGAAAGGCTGGAGTACATGAGGAGCTCATTTATCTGGTACTCTGACACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 ACGCCGCTCTTCCAAAGCCAGGTCACCATCTCAGTGCAGAACGTCGACACTGCTAC 240
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 TTGCATGAGAGCAGTCTGAAGCCCTCGACAGCGCCGTGATTTGTGTGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHisTrpGly 120
 Db 301 GTGGGATATTGCGAGTATGTTCCAACTGCGCAAGTGGCTGAATATTCCAGCATTTGGGC 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 361 CAGGGCACCCCTGTCACCGTCTCTCA 387

RESULT 3

AAD32665
 ID AAD32665 standard; DNA; 807 BP.

XX AAD32665;

AC 29-AUG-2003 (revised)
 DT 18-JUN-2002 (first entry)

XX Chimeric SCBP C6ML3-9 sFV' DNA.

XX Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
 KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
 KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX Key

FT CDS Location/Qualifiers
 FT 1..807
 FT /tag= a
 FT /product= "Chimeric SCBP C6ML3-9 sFV' protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial

XX WO200200914-A2.

XX 03-JAN-2002.

XX 25-JUN-2001; 2001WO-US020182.

XX 23-JUN-2000; 2000US-0213653P.

XX (HUST/) HUSTON J S.

XX (WILS/) WILS P.

XX (QUAN/) QUAN Z.

XX (LAUR/) LAURENT O.

XX (MARA/) MARASCO W A.

XX (SCHE/) SCHERMAN D.

PI Huson JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;

XX MPI; 2002-268789/31.

XX Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
 PT residue.

XX Disclosure; Fig 6; 96pp; English.

XX The invention relates to gene-delivery compound comprising a single-chain
 CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6ML3-9 sFV' DNA
 CC comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)

XX SQ Sequence 807 BP; 160 A; 240 C; 237 G; 170 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,97e-63	Length:	807
Score:	694.00	Matches:	127
Percent Similarity:	100.0%	Conservative:	2
Best Local Similarity:	98.4%	Mismatches:	0
Query Match:	99.1%	Indels:	0
DB:	6	Gaps:	0

US-10-092-640-32 (1-129) x AAD32665 (1-807)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLeuLysProGlyGlnSerLeuLysIle 20
 Db 1 CAGGTCACTGTTGACAGTCTGGGGCAGAGTTGAAAAAACCAGGAGTCTCGAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 Db 61 TCCTGTAAGGGTTCGTGATACACCTTACACGCTTACCTGAGTCCCTGGGCGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGlnLysTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
 Db 121 CCGGGAAAGGCTGGAGTACATGAGGAGCTCATTTATCTGGTACTCTGACACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 ACGCCGCTCTTCCAAAGCCAGGTCACCATCTCAGTGCAGAACGTCGACACTGCTAC 240
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 TTGCATGAGAGCAGTCTGAAGCCCTCGACAGCGCCGTGATTTGTGTGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHisTrpGly 120
 Db 301 GTGGGATATTGCGAGTATGTTCCAACTGCGCAAGTGGCTGAATATTCCAGCATTTGGGC 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 361 CAGGGCACCCCTGTCACCGTCTCTCA 387

RESULT 4

AAD32666
 ID AAD32666 standard; DNA; 846 BP.

XX AAD32666;

XX 29-AUG-2003 (revised)

XX 18-JUN-2002 (first entry)

XX Chimeric SCBP C6ML-3-sFV' -LI-KDEL DNA.

XX Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
 KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
 KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.

```

XX OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX Key Location/Qualifiers
FH CDS 1..846
FT /tag= a
FT /product= "Chimeric SCBP C6ML-3-9sfv'-L1-KDEL protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX MO200200914-A2.
XX PN 03-JAN-2002.
XX PD
XX PF 25-JUN-2001; 2001WO-US020182.
XX PR 23-JUN-2000; 2000US-0213653P.
XX PA (HUST/) HUSTON J S.
XX PA (WILS/) WILS P.
XX PA (QUAN/) QUAN Z.
XX PA (LAUR/) LAURENT O.
XX PA (MARA/) MARASCO W A.
XX PA (SCHE/) SCHERMAN D.
XX PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX DR WPI; 2002-268789/31.
XX DR P-PSDB; AAE20409.
XX PT Gene-delivery compound for targeted gene delivery, comprises single-chain
XX PT binding polypeptide having effector segment with cysteinyl residue and
XX PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX PT residue.
XX PS Example 2; Fig 8; 96pp; English.
XX CC The invention relates to gene-delivery compound comprising a single-chain
XX CC binding polypeptide (SCBP) having at least one effector segment having a
XX CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
XX CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
XX CC compound is useful for targeted gene delivery for treating diseases by
XX CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9sfv'-L1-KDEL
XX CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
XX CC standardise OS field)
XX SQ Sequence 846 BP; 171 A; 250 C; 246 G; 179 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,09e-63 Length: 846
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 6 Gaps: 0

US-10-092-640-32 (1-129) x AAD32666 (1-846)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuValysProGlyGluSerLeuValSile 20
Db 1 CAGGTCACACTGTCAGTCGTGGGGCAGAGGTAAAAACCCGGGAGTCCTCGAAGATC 60
QY 21 SerGylsGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 TCCTGTAAAGGGTTCGTGATACAGCTTACACAGCTACTGATCGCCGTGGGTCGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyLysSerSerThrLysTyr 60
Db 121 CCCGGGAAAGGCTTGAGTACAGAGGGGCTCATCTATCTCGGTACTACACCAATATAC 180
QY 61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80

```

```

Db 181 ACCCGCTCTTCCAAAGCCAGGTCAACCATCTAGTCGACACATCCGTCAGCACTGCTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
Db 241 TTGCATATGAGCAGTCTGAGAGCCCTCGGACAGCCGCTGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db 301 GTGGATATTGTCAGTATTCACACTGCGCAAGTGGCCGTAATACTTCCAGCATTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
Db 361 CAGGGCACCCCTGTCACCGCTCTCTCA 387

RESULT 5
AAD32667
ID AAD32667 strand; DNA; 861 BP.
XX
XX AC AAD32667;
XX DT 29-AUG-2003 (revised)
XX DT 18-JUN-2002 (first entry)
XX DE Chimeric SCBP C6ML-3-9sfv'-L2-KDEL DNA.
XX KW Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
XX KW nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
XX KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX OS Homo sapiens.
XX OS Mus sp.
XX OS Chimeric.
XX FH Key Location/Qualifiers
FH FT 1..861
FT CDS /tag= a
FT /product= "Chimeric SCBP C6ML-3-9sfv'-L2-KDEL protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX MO200200914-A2.
XX PN 03-JAN-2002.
XX PD 25-JUN-2001; 2001WO-US020182.
XX PF 23-JUN-2000; 2000US-0213653P.
XX PR 23-JUN-2000; 2000US-0213653P.
XX PA (HUST/) HUSTON J S.
XX PA (WILS/) WILS P.
XX PA (QUAN/) QUAN Z.
XX PA (LAUR/) LAURENT O.
XX PA (MARA/) MARASCO W A.
XX PA (SCHE/) SCHERMAN D.
XX PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX DR WPI; 2002-268789/31.
XX DR P-PSDB; AAE20410.
XX PT Gene-delivery compound for targeted gene delivery, comprises single-chain
XX PT binding polypeptide having effector segment with cysteinyl residue and
XX PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX PT residue.
XX PS Example 2; Fig 10; 96pp; English.
XX CC The invention relates to gene-delivery compound comprising a single-chain
XX CC binding polypeptide (SCBP) having at least one effector segment having a
XX CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
XX CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
XX CC compound is useful for targeted gene delivery for treating diseases by

```


CC Gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFV'-L2-KDEL
CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 861 BP; 173 A; 255 C; 250 G; 183 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,13e-63 Length: 861
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 6 Gaps: 0
US-10-092-640-32 (1-129) x AAD32667 (1-861)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
Db 1 CAGGTGACAGTGTGTGAGTCTGGGGCAGAGGTAAAGCCGGGAGTCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 TCCTGTAAAGGTTCTGATACAGCTTACCACTGATCGCTGGGTCGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 121 CCGGGAAAGGCTTGAGTACATGGGGCTCATATCTGCTGACTGACACCAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 AGCCGCTCTTCCAAAGCCAGGTACACATCTCAGTGCAGACAGCCGTCAGACTGCTAC 240
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 TTGCATGTAGAGCAGTCTGAAGCCCTCGACAGCGCGTGTATTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerAsnGlyAlaGlyTrpProGlyLysPheGlnHisTrpGly 120
Db 301 GTGGGATATTGCAAGTATCCAACTGCGCAAAAGTGGCTGAAATATTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
Db 361 CAGGGCACCTGTGTCACCGTCTCTCA 387
RESULT 6
AAD32669
ID AAD32669 standard; DNA; 873 BP.
XX
AC AAD32669;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE Chimeric SCBP C6ML-3-9sFV'-L2-nls DNA.
XX
KM Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KM nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KM gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS
FH Key Location/Qualifiers
FT 1..873
FT /*tag= a
FT /product= "Chimeric SCBP C6ML-3-9sFV'-L2-nls protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
XX WO200200914-A2.
XX
PD 03-JAN-2002.

XX
XX 25-JUN-2001; 2001MO-US020182.
XX
XX
XX 23-JUN-2000; 2000US-0213653P.
XX
XX (HUST/) HUSTON J S.
XX (WILS/) WILS P.
XX (QUAN/) QUAN Z.
XX (LAUR/) LAURENT O.
XX (MARA/) MARASCO W A.
XX (SHE/) SCHERMAN D.
XX
XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX WPI; 2002-268789/31.
XX P-PSDB; AAE20412.
XX
XX Gene-delivery compound for targeted gene delivery, comprises single-chain
XX binding polypeptide having effector segment with cysteinyl residue and
XX nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX residue.
XX
XX Example 2; Fig 14; 96pp; English.
XX
XX The invention relates to gene-delivery compound comprising a single-chain
XX binding polypeptide (SCBP) having at least one effector segment having a
XX cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
XX associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
XX compound is useful for targeted gene delivery for treating diseases by
XX gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFV'-L2-nls
XX DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
XX standardise OS field)
SQ Sequence 873 BP; 177 A; 260 C; 252 G; 184 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,17e-63 Length: 873
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 6 Gaps: 0
US-10-092-640-32 (1-129) x AAD32669 (1-873)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
Db 1 CAGGTGACAGTGTGTGAGTCTGGGGCAGAGGTAAAGCCGGGAGTCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 TCCTGTAAAGGTTCTGATACAGCTTACCACTGATCGCTGGGTCGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 121 CCGGGAAAGGCTTGAGTACATGGGGCTCATATCTGCTGACTGACACCAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 AGCCGCTCTTCCAAAGCCAGGTACACATCTCAGTGCAGACAGCCGTCAGACTGCTAC 240
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 TTGCATGTAGAGCAGTCTGAAGCCCTCGACAGCGCGTGTATTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerAsnGlyAlaGlyTrpProGlyLysPheGlnHisTrpGly 120
Db 301 GTGGGATATTGCAAGTATCCAACTGCGCAAAAGTGGCTGAAATATTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
Db 361 CAGGGCACCTGTGTCACCGTCTCTCA 387

RESULT 7

AA032668
ID AAD32668 standard; DNA; 888 BP.
XX
AC AAD32668;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE Chimeric SCBP C6ML-3-9sfv'-L2-H14 DNA.
XX
KW Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KW nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..888
FT /tag= a
FT /product= "Chimeric SCBP C6ML-3-9sfv'-L2-H14 protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN WO200200914-A2.
XX
PD 03-JAN-2002.
XX
PF 25-JUN-2001; 2001WO-US020182.
XX
PR 23-JUN-2000; 2000US-0213653P.
XX
PA (HUST/) HUSTON J S.
PA (WILS/) WILS P.
PA (QUAN/) QUAN Z.
PA (LAUR/) LAURENT O.
PA (MARA/) MARASCO W A.
PA (SCHE/) SCHERMAN D.
XX
PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
DR WPI: 2002-268789/31.
DR P-PSDB; AAE20411.
XX
PT Gene-delivery compound for targeted gene delivery, comprises single-chain
PT binding polypeptide having effector segment with cysteinyl residue and
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
PT residue.
XX
PS Example 2; Fig 12; 96pp; English.
XX
CC The invention relates to gene-delivery compound comprising a single-chain
CC binding polypeptide (SCBP) having at least one effector segment having a
CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
CC compound is useful for targeted gene delivery for treating diseases by
CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9sfv'-L2-H14
CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 888 BP; 187 A; 263 C; 257 G; 181 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,22e-63 Length: 888
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: Gaps: 0

US-10-092-640-32 (1-129) x AAD32668 (1-888)

QY 1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysLysProGlyGluSerLeuLysIle 20
Db 1 CAGGTGACAGCTGGTCAGTCTGGGGCAGAGTGAAGAAAAAGCCGGGAGCTCTGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 TCCTGTAAAGGTTCTCGATACAGCTTTACAGACTACTGGATGCGCTGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysPheSerThrLysTyr 60
Db 121 CCCGGGAAAGGCGCTGAGACATGGGGCTCATCTCTCTGGGACTCTGACACCAAAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrLysTyr 80
Db 181 AGCCCGCTCTTCAGAGCCAGGTCAACATCTCAGTCAGACAACTCCGTACGACTGCTGC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 TTGCAATGGAGCAGCTGAAGCCCTCGGACAGCGCGGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
Db 301 GTGGGATATTGGCAGTAGTTCACAACTGCGCAAGTGGCTGAAATACCTCCAGCATTTGGGCG 360
QY 121 GlnGlyThrIleValThrValSerSer 129
Db 361 CAGGGCACCTGTGTCAACCGTCTCTCA 387

RESULT 8

AA03465
ID AAS03465 standard; cDNA; 387 BP.
XX
AC AAS03465;
XX
DT 29-AUG-2001 (first entry)
XX
DE DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 53.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW heart disease; complementarity determining region; CDR; ss.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI: 2001-282031/29.
DR P-PSDB; AAU02565.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS Disclosure; Page 133; 182pp; English.

XX
XX AAS03401-AA03535 represent anti-adipocyte monoclonal antibody heavy and
XX light chain coding sequences of the invention. The antibodies can be used
XX in the treatment of obesity and obesity related diseases. The antibodies
XX can be used to deliver drugs or pro-drugs directly to the fat mass of an
XX obese patient or the antibody can be used as a therapeutic itself.
XX Antibodies binding specifically to adipocytes can be used to activate the
XX immune system to destroy the cells by complement mediated lysis. The
XX antibodies may be labeled with a detectable label such as radiolabel,

```
RESULT 9
ID AEE03776 standard; DNA; 364 BP.
XX AC AEE03776;
XX DT 26-JAN-2006 (first entry)
XX DE Antibody 015-126 VH nucleotide sequence SEQ ID NO:102.
XX KM antibody production; cytostatic; diagnosis; cancer;
XX heavy chain variable region; coding sequence; ds.
OS Synthetic.
```

	Location/Qualifiers
Key	l..363
CDS	/tag= a /partial /product= "Antibody 015-126 VH amino acid sequence"

```
PB JP2005185281-A.  
XX PN  
XX PD 14-JUL-2005.
```

Qy	1	GlnValAlaGlnLeuLeuGlnSerGlyValAlaGlnLeuLysProGlyGlnSerLeuLysIle	20
Db	1	CAAGTGCACCTGATGCTCAGCTTCGACACCAAGGTGAAAAAGCCGGGAGAGTCTTGAAATC	60
Qy	21	SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTyrValArgGlnMet	40
Db	61	TCTCTGAAGGGTTCTGGATACAGCTTTCACAGCTACGTGAGTGGCTGGTCCGCCAATG	120
Qy	41	ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr	60
Db	121	CCCGGGAAAGCCCTGAGTGGATGGAGTATCATCTCTGGTACTCTGATACCAAGATAC	180
Qy	61	SerProSerPheGlnGlyGlnValThrTlIeSerValAspLysSerValSerThrAlaTyr	80
Db	181	AACCCGCTCCTTCCAAAGGCGCAGGTACCCATCTCCACGCCACAAGTCCATACACACCGCCTAC	240
Qy	81	LeuGlnTyrPserSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp	100
Db	241	CTGCAGGTGAGAGGCTTAAAGCCCTCGGACACCCGCCATGATATTACTGTGGAGACTTACT	300
Qy	101	ValGlyTyrCysSerSerSerAspCysAlaLysTrpProGlnTyrPheGlnIleStrpGly	120
Db	301	TTCCTCTTATGACGAGAC-----TGGTTTGACTACTGGGCG	336
Qy	121	GlnGlyThrLeuValThrValSerSer	129

```

Db          337 CAGGGAACCTGCTACCGCTCTCGAGC 363
RESULT 10
AAF61513
XX AAF61513 standard; DNA; 906 BP.
AC AAF61513;
XX
XX
XX 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry)
XX
XX
DE DNA encoding SNV-env leader/human 6C3-scfv fusion construct.
XX
XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
KM cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KM gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KM acquired immune deficiency syndrome; severe combined immune deficiency;
KM T cell lymphoma; fusion construct; ds.
XX
OS Homo sapiens.
OS Spleen necrosis virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..135
FT /tag= a
FT /product= "SNV-env leader peptide"
FT /note= "No stop codon given"
FT CDS 136..906
FT /tag= b
FT /product= "7B4-scfv"
FT /note= "no stop codon given"
FT /partial
XX
XX DE19946142-A1.
XX
XX 29-MAR-2001.
XX
XX 27-SEP-1999; 99DE-01046142.
XX
XX 27-SEP-1999; 99DE-01046142.
XX
XX (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
XX Cichutek K, Engelstaedter M;
XX
XX MPI; 2001-246140/26.
XX
XX P-PSDB; AAB70844.
XX
XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
XX of e.g. acquired immune deficiency syndrome, encodes a single-chain
XX variable antibody fragment.
XX
XX Claim 1, Fig 5, 18pp; German.
XX
XX This invention describes a novel cell-targeting vector (A) containing a
XX DNA sequence (1) encoding a single-chain variable antibody fragment
XX (scFv). The products of the invention have antiviral, cytostatic and
XX immunostimulant activity and can be used in gene therapy, immunization
XX and diagnosis particularly of T cell-associated diseases, specifically
XX acquired immune deficiency syndrome (AIDS), severe combined immune
XX deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
XX of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
XX human B cells, and 1000 fold selectivity over other human cells. A vector
XX designated 7A5 encodes a 329 amino acid single-chain variable antibody
XX fragment, fully defined in the specification. It was used to transform
XX D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
XX (SNV)) cells, C816 (human T lymphocyte) cells, and HeLa (human cervical
XX carcinoma) cells. After 48 hours, the cells were stained with X-gal to
XX determine transfection. The viral titer (infectious units/ml) was over
XX 1 million for D17, 1 million for C816 but less than 100 for HeLa,
XX showing the high selectivity for human T cells. This sequence encodes the

```

```

CC SNV-env leader/human 6C3-scfv fusion construct used in the construction
CC of novel cell targeting vectors described in the invention. (Updated on
CC 11-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 906 BP; 204 A; 246 C; 262 G; 194 T; 0 U; 0 Other;
XX
XX
Alignment Scores:
Pred. No.: 3.54e-47 Length: 906
Score: 540.00 Matches: 102
Percent Similarity: 88.4% Conservative: 12
Best Local Similarity: 79.1% Mismatches: 13
Query Match: 77.1% Indels: 2
DB: 5 Gaps: 2
XX
US-10-092-640-32 (1-129) x AAF61513 (1-906)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysile 20
DB 142 CAGGTACAGCTCAGACAGTCAGAGCAGAAATGAAAGCCCGGGAGCTCTGAAAATC 201
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
DB 202 TCCTGTAAAGGCTTTGGATACGACTTTAGCACTTACCTGATGCGCTGGGTGGCAGAGT 261
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
DB 262 CCGGGAAAGGCGCTGAGTACAGGAGCTCACTTCTCGTACTCTGACACCAATAC 321
QY 61 SerProSerPheGlnGlyAlaValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 322 AGCCCGCTCTTCMAAGGCCAGGTCACCACTCTCAGCGCAAGTCCATCGACGACCGCTAC 381
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
DB 382 CTGCAGTGAAGCAGCGCTGAAAGCCTCGGACACCGCCATGATTACTATCGAGACTCTCT 441
QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHis--Trp 119
DB 442 ---GGATATTGTAGTAGTACGCTGCTAGTACTGCTACTACTACTACTACTGACGCTCTG 498
QY 120 GlyGlnGlyThrLeuValThrValSer 128
DB 499 GGC CGGGGAACCTGCTGACCGCTCTG 525
XX
RESULT 11
AEB01074
XX ID AEB01074 standard; DNA; 369 BP.
XX
XX AEB01074;
XX
XX 08-SEP-2005 (first entry)
XX
XX Human IP10 antibody heavy chain variable region DNA, SEQ ID NO 102.
XX
XX antibody; IP-10; inflammation; immune disorder; dermatological disease;
XX respiratory disease; neurological disease; degeneration; infection;
XX Neutrophilic; Antiarrhythmic; Antirheumatic; Antiinflammatory;
XX Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;
XX Antidiabetic; Antiproliferative; Antihypertensive; Anticancer;
XX Respiratory-Gen.; Cerebroprotective; Vasodilator; Nootropic;
XX Antiparkinsonian; Antiangiogenic; Antiartherosclerotic; Virocidic;
XX Antibacterial; heavy chain variable region; ds; gene.
XX
XX Homo sapiens.
XX
XX WO2005058815-A2.
XX
XX 30-JUN-2005.
XX
XX 10-DEC-2004; 2004WO-US041506.
XX
XX 10-DEC-2003; 2003US-0529180P.
XX

```

PA (MEDA-) MEDAREX INC.
 XX Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
 XX WPI: 2005-467095/47.
 DR P-PSDB; ABB01010.
 XX
 PT Isolated human monoclonal antibody or an antigen-binding portion, which
 PT specifically binds to human interferon gamma inducible protein 10 (IP-
 PT 10), useful for treating viral or bacterial infection, or inflammatory or
 PT autoimmune diseases.
 XX
 PS Disclosure; SEQ ID NO 102; 179pp; English.
 XX
 CC The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human IPAC. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type 1 diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
 CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), glaucoma,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC glomerulonephritis, rapidly progressive glomerulonephritis, or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the human IP10 monoclonal antibody heavy chain
 CC variable region DNA.
 XX
 SQ Sequence 369 BP; 76 A; 105 C; 110 G; 78 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,48e-47 Length: 369
 Score: 539.00 Matches: 101
 Percent Similarity: 89.9% Conservative: 15
 Best Local Similarity: 78.3% Mismatches: 7
 Query Match: 77.0% Indels: 6
 DB: 14 Gaps: 3
 US-10-092-640-32 (1-129) x ABB01074 (1-369)
 QY 1 GlnValGlnLeuLengInSerGlyAlaGluLeuValProGlyGluSerLeuValle 20
 Db 1 GAGGGGCACTGCTGAGTCTGAGGAGGTAAGCCCGGGAGTCTGAAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrIserPheThrSerTyrTyrIleAlaTyrValArgInmet 40
 Db 61 TCTCTGAAGGGTTTCGATACAACTTCCAGGTATGATGGCGGTGGCCGAGATG 120
 QY 41 ProGlyLysGlyLeuGluTyrIleGlyLeuLeuTyrProGlyLysSerAspThrIleTyr 60
 Db 121 CCCGGGAAAGGCGCTGAGTGGATGGGGGTCATCTCCCGGAGCTCATATACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 ACCCGCTCTTCCAGGCCAAGTCACTCATCCAGCCGCAAGTCCATCCAGCCGCTTAC 240
 QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 CTGAGTGGAGCAGCCTGAAAGGCGCTCGACACCGCATGATATCTGTCGAGA----- 294

QY 101 ValGlyTyrCysSerSerPheGlnValTyrProGlyTyrPheGlnHisTyrGly 120
 Db 295 ---GGATATATTGATGGTGGTACTGCTC-----TACCCTA---TTCTTCCAGTACTGGGCGC 342
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 343 CAGGGCACCTCTGTCTCCGTTCTCTCC 369
 RESULT 12
 ID ABB274803
 AB274803 standard; DNA; 660 BP.
 XX
 AC AB274803;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human anti-TIMP-1 antibody heavy chain #30 DNA.
 XX
 KW Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;
 KW matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatotropic;
 KW variable light chain; cytosolic; nephrotropic; cardiant; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer; gene; ss;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN W0200286085-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002WO-US012801.
 XX
 PR 24-APR-2001; 2001US-0285683P.
 XX
 PA (PARB) BAYER CORP.
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
 DR WPI: 2003-129114/12.
 P-PSDB; ABB01532.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
 PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
 PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
 PT cancer.
 XX
 PS Claim 34; Page 203; 228pp; English.
 XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
 CC -1. The antibody comprises a variable heavy chain (VHCDR3 region and a
 CC variable light chain (VLCDR3 region). An antibody preparation of the
 CC invention has hepatotropic, cytosolic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in AB274774-AB274816 encode the heavy chain regions of a
 CC human anti-TIMP-1 antibody of the invention
 XX
 SQ Sequence 660 BP; 161 A; 164 C; 196 G; 139 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9.04e-47 Length: 660
 Score: 534.50 Matches: 99
 Percent Similarity: 86.0% Conservative: 12

11

KW variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis.

```

SQ      Sequence 666 BP, 164 A, 163 C, 197 G, 142 T, 0 U, 0 Other:
+
Alignment Scores:
Pred. No.:      1,48e-46      length:      666
Score:          532.50        Matches:      100
Percent Similarity: 87.6%      Conservative: 13
Best Local Similarity: 77.5%      Mismatches:  7
Query Match:    76.1%         Indels:      9
DB:             10           Gaps:        2
US-10-092-640-32 (1-129) x AB274798 (1-666)

```

KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KM lupus nephritis; glomerulosclerotic renal disease; lung cancer; gene; ss;
 KM idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX MO200286085-A2.
 PN
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002MO-US012801.
 XX
 PR 24-APR-2001; 2001US-0285683P.
 XX
 PA (FARB) BAYER CORP.
 PI (MORP-) MORPHOSYS AG.
 PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
 XX
 DR MPI: 2003-129114/12.
 DR P-PSDB; ABR01542.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
 PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
 PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
 PT cancer.
 XX
 PS Claim 34; Page 205-206; 228pp; English.
 XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
 CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
 CC variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in AB274774-AB274816 encode the heavy chain regions of a
 CC human anti-TIMP-1 antibody of the invention
 CC
 XX
 SQ Sequence 666 BP; 163 A; 164 C; 197 G; 142 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1.48e-46 Length: 666
 Score: 532.50 Matches: 101
 Percent Similarity: 84.8% Conservative: 11
 Best Local Similarity: 76.5% Mismatches: 5
 Query Match: 76.1% Indels: 15
 DB: 10 Gaps: 2
 US-10-092-640-32 (1-129) x AB274810 (1-666)
 QY 1 GlnValGlnIleuLeuGlnSerGlyAlaGluLeuLysLeuProGlyGlnSerLeuLysIle 20
 DB 1 CAGGTGCAATTGGTTTCAGAGCGCGCGGAAGTGAATAAAACCGGGCGAAACCTGAAATTT 60
 QY 21 SerCysLeuGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 DB 61 AGCTGCAGAAAGCTCCGATATTCCTTTACAGACTATTGGATTGGCTGGCGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGlnIleuLeuMetGlyLeuIleTyrProGlyLysSerAspTrpLysTyr 60
 DB 121 CTGGGAAGGGCTTCAGAGTGAAGGCGCATTTATTCGGGCGAATGCGGTACCGGTAT 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 181 TCTCCAGAGCTTTCAGGGCCAGTGAACCATTAAGCGGATTAAGCATTTAGCACCGGTAT 240

QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 DB 241 CTTCATGAGGAGCGCTCGAAGAGCGAGACGCGCATGATTTATTCGGCGCT- 294
 QY 101 ValGlyTyrCysSerSerSerSerAlaValTyrTrpProGlu-----TyrPheGln 117
 DB 295 -----CTTATCTGAGGATCTTATTTATTTGAT 324
 QY 118 HisTrpGlyGlnGlyThrLeuValThrValSerSer 129
 DB 325 TATTGGGGCCAGACACCTGTGACGCTTACTCA 360
 RESULT 15
 AB274813
 ID AB274813 standard; DNA; 672 BP.
 XX
 AC AB274813;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human anti-TIMP-1 antibody heavy chain #40 DNA.
 XX
 DE Human: antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;
 KM matrix metalloproteinase; MMP; variable heavy chain; VHC; DR3; hepatotropic;
 KM variable light chain; cytosstatic; nephrotropic; cardiant; liver fibrosis;
 KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KM lupus nephritis; glomerulosclerotic renal disease; lung cancer; gene; ss;
 KM idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200286085-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002MO-US012801.
 XX
 PR 24-APR-2001; 2001US-0285683P.
 XX
 PA (FARB) BAYER CORP.
 PI (MORP-) MORPHOSYS AG.
 PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
 XX
 DR MPI: 2003-129114/12.
 DR P-PSDB; ABR01542.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1) antibodies,
 PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
 PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
 PT cancer.
 XX
 PS Claim 34; Page 207; 228pp; English.
 XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of TIMP
 CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
 CC variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
 CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
 CC sequences shown in AB274774-AB274816 encode the heavy chain regions of a
 CC human anti-TIMP-1 antibody of the invention
 CC
 XX
 SQ Sequence 672 BP; 162 A; 164 C; 198 G; 148 T; 0 U; 0 Other;
 SQ

Alignment Scores:

Pred. No.:	1.5e-46	Length:	672
Score:	532.50	Matches:	102
Percent Similarity:	86.8%	Conservative:	10
Best Local Similarity:	79.1%	Mismatches:	10
Query Match:	76.1%	Indels:	7
DB:	10	Gaps:	2

US-10-092-640-32 (1-129) x ABZ74813 (1-672)

```

QY      1  GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysProGlyValSerLeuLysIle 20
      1  CAGGTCCAAATTGGTTCAGAGCGCGCGAGTAGTAAACCGGCGAAGCCCTGAAATTT 60
      21  SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      61  AGCTGCAAAGGTTCCGGATATTCCTTTACGAGCTATTGGATTGGCTGGGTGGCCAGATG 120
QY      41  ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
      121  CCTGGGAAGGCTCTCGAGGATGGGCAATTATTATCCGGCGCATAGCATACCGCTTAT 180
QY      61  SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      181  TCTCCAGCTTTCAGGGCCAGTGACCATTTAGCGCGGATTAAGCATTAACCGCGCTAT 240
QY      81  LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
      241  CTTCAATGAGCAGCCTGAAGCGAGCATACGGCATGATATTATGCGGCGCTTT--- 297
QY      101  ValGlyTyrCysSerSerSerSerAlaLysTrpProGlnTyrPheGlnHisTrpGly 120
      298  GTTCTTAATAANGTTCT-----GTTCCCTATTATTGATTATTTGGGCGC 339
DB
QY      121  GlnGlyThrLeuValThrValSerSer 129
      340  CAAAGCACCCCTGGTGAACGTTAGCTCA 366
DB

```

Search completed: May 25, 2006, 16:28:23
 Job time : 552.862 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:28:39 ; Search time 4241.95 Seconds

(without alignments)
2550.806 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700
Sequence: 1 QVQLQSGAELEKKGESLKI.....AKMPYFQHWGQSTLVTVSS 129

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=x1h
-O=/abs/ABSWEB.spool/US10092640/runat_25052006.155716.5880/app.query.fasta_1
-DB=EST -QFMT=fastcap -SUFFIX=est -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=adbs05h
-USER=US10092640@CGN_1_1.7986@runat_25052006.155716.5880 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6 -FCGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_esc1: *
2: gb_esc3: *
3: gb_esc4: *
4: gb_esc5: *
5: gb_esc6: *
6: gb_esc7: *
7: gb_esc8: *
8: gb_esc9: *
9: gb_esc10: *
10: gb_esc11: *
11: gb_esc12: *
12: gb_esc13: *
13: gb_esc14: *
14: gb_esc15: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	77.1	658	3	BM713153 UI-E-EJO-
2	527.5	75.4	857	2	BI906125 603062533
3	526.5	75.2	843	2	BG754240 602709791
4	524	74.9	1114	3	BM920470 AGENCOURT

5	523.5	74.8	573	9	DA978565	DA978565
6	523.5	74.8	795	2	BG685604	BG685604 602637582
7	522.5	74.8	873	2	BG754454	BG754454 602710060
8	522.5	74.6	536	6	DA988840	DA988840
9	520	74.3	607	2	BG755575	BG755575 602716258
10	516.5	73.8	568	9	DA988827	DA988827
11	515.5	73.6	875	3	BQ711293	BQ711293 AGENCOURT
12	515	73.5	573	9	DA981607	DA981607
13	514.5	73.5	530	9	DB190036	DB190036
14	514.5	73.5	584	2	DA969213	DA969213
15	513	73.3	862	7	BF663762	BF663762 602145490
16	512.5	73.2	476	9	DB109549	DB109549
17	511.5	73.1	556	9	DA954699	DA954699
18	509.5	72.8	438	7	AM402496	AM402496 UI-HF-BKO
19	509.5	72.8	921	3	BQ710635	BQ710635 AGENCOURT
20	506.5	72.4	487	7	AM403158	AM403158 UI-HF-BKO
21	506.5	72.4	777	2	BG754281	BG754281 602709838
22	503	71.9	511	9	DA962753	DA962753
23	502.5	71.8	566	9	DA930979	DA930979
24	502	71.7	565	9	DA977102	DA977102
25	501	71.6	957	3	BQ709811	BQ709811 AGENCOURT
26	500	71.4	559	9	DA984100	DA984100
27	499.5	71.4	444	7	AM401565	AM401565 UI-HF-BKO
28	499	71.3	880	3	DB115918	DB115918
29	498.5	71.2	880	3	BQ712042	BQ712042 AGENCOURT
30	498	71.1	511	9	DA930878	DA930878
31	495	70.7	545	9	DA979866	DA979866
32	493.5	70.5	520	9	DA429338	DA429338
33	493.5	70.5	863	2	BG756025	BG756025 602716515
34	492.5	70.4	652	2	BG757902	BG757902 602714934
35	492.5	70.4	905	2	BG686261	BG686261 602638145
36	492	70.3	754	9	DA581067	DA581067
37	491.5	70.2	571	9	DA986278	DA986278
38	491.5	70.2	581	9	DA968943	DA968943
39	490	70.0	579	9	DB113736	DB113736
40	489	69.9	579	9	DA431367	DA431367
41	488	69.7	591	5	CD705168	CD705168
42	487.5	69.6	835	2	BM007733	BM007733
43	487	69.6	569	9	DA428868	DA428868
44	486.5	69.5	554	9	DA966706	DA966706
45	486.5	69.5	574	9	DB111424	DB111424

ALIGNMENTS

RESULT 1
BM713153
LOCUS
DEFINITION
UI-E-EJO-ahn-d-09-0-UI-r1 UI-E-EJO Homo sapiens cDNA clone
BM713153
ACCESSION
BM713153
VERSION
BM713153.1 GI:19026411
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 658)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reegen.com).
Seq primer: M13 Reverse.

FEATURES

source 1..658
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJO-ahn-d-09-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1ib="UI-E-EJO"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJO is a subcloned cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGANTCAGAGA; lens, CGATTAGGGA; eye anterior segment,
AATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG;
Foveal and Macular, GTCC; RPE and Choroid, ACCCA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:

Pred. No.: 2 31e-51 Length: 658
Score: 540.00 Matches: 99
Percent Similarity: 88.4% Conservative: 15
Best Local Similarity: 76.7% Mismatches: 11
Query Match: 77.1% Indels: 4
DB: 3 Gaps: 1

US-10-092-640-32 (1-129) x BM713153 (1-658)

```

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 64 GAGGTGCACCTGGTCCAGTCTGGAGCAGAGTGAATAAAGCCGGGAAATCTCGAAGATC 123
QY 21 SerCysIlyGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 124 TCCTGTAAAGCTTCTGATACAGGTTTACACCTACGAGGCTGCGCTGGTGGCCAGG 183
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 184 CCGGGAAAGGCTGAGTGGATGGGATCATCTATCTCGTGATCTCCATACCAATAC 243
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 244 AGTCGCTCTCCCAAGGCCAGGTCAACATTTCAGCGCAAGCCATCAGTACCGGCTTCA 303
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 304 CTGCACTGAGAGCAGCTGGAAGGCTTGGACACCGCCCTGATTTCTGTGCGAGACATCGT 363
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLysPheGlnHisTrpGly 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 364 ATTGATATTGTAGTCGTTCTTACTCTCTCTCG-----ACTGACTACTGGGGC 411
QY 121 GlnGlyThrLeuValThrValSerSer 129
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 412 CAGGGAACCTGGTCAACGCTCTCTCTCA 438

```

RESULT 2
BI906125 857 bp mRNA linear EST 16-OCT-2001
LOCUS 603062533F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211561 5',
DEFINITION mRNA sequence.

ACCESSION BI906125.1 GI:16168777
VERSION BI906125
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE 1 (bases 1 to 857)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM11531 row: b column: 10
High quality sequence stop: 738.

FEATURES

source

1..857
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5211561"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 9 18e-50 Length: 857
Score: 527.50 Matches: 99
Percent Similarity: 85.3% Conservative: 11
Best Local Similarity: 76.7% Mismatches: 12
Query Match: 75.4% Indels: 7
DB: 2 Gaps: 1

US-10-092-640-32 (1-129) x BI906125 (1-857)

```

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 91 GAGGTGCACCTGGTCCAGTCTGGAGCAGAGTGAATAAAGCCGGGAGTCTCGAAGATC 150
QY 21 SerCysIlyGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 151 TCCTGTAAAGCTTCTGATACAGGTTTACACCTACGATCTCGTGGTGGCCAGATG 210
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 211 CCGGGAAAGGCTGAGTGGATGGGATCATCTATCTCGTGATCTCGATCCAGATAC 270
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

Db	271	AGCCCGTCCTTCAGAGGCGAGGTACACATCTCAGCGACCAAGTCATCAGACCGCCCTAC	330
QY	81	LeuGlnTyrPseSerLeuLysProSerIlePseSerAlaValTyrPheCysAlaArgHisasp	100
Db	331	CTGCAGTGGAGCAGCTCTGAAGGCGCTCGGACACCGCCATGTATTACTGTGCGAGACACGAG	390
QY	101	ValGlyTyrCysSerSerSerasnCysAlaLysTyrProGluTyrPheGlnHisIlePgly	120
Db	391	CAGTGGCTGGTACGAGACGAAGTGGG-----TTGACCCCTGGGGG	429
QY	121	GlnGlyThrIleuValThrValSerSer	129
Db	430	CAGGAAACCTGGTCACCGCTCTCTCA	456
RESULT 3			
BG754240			
LOCUS	843	bp	mRNA
DEFINITION	6027079191	NIH_MGC_48	Homo sapiens CDNA clone IMAGE:4846102 5',
ACCESSION	BG754240		
VERSION	BG754240.1	GI:14064893	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
	1 (bases 1 to 843)		
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT			

ORIGIN

Alignment Scores:

Pred. No.:	1.17e-49	Length:	843
Score:	526.50	Matches:	99
Percent Similarity:	86.8%	Conservative:	13
Best Local Similarity:	76.7%	Mismatches:	12
Query Match:	75.2%	Indels:	5
DB:	2	Gaps:	1

US-10-092-640-32 (1-129) X BG754240 (1-843)

QY 1 GlnValGlnLeuGlnSerGlyAlaGluLeuLysLysProGlyGlnSerLeuLysIle 20

Dd		59	GAGGTGCACGCTGGTGCAGTCTGGAGCAGAGGTGA AAAAGCCCGGGAGATCTCTGAAGTC	118
Oy		21	SerCysIysglYserGIlyrSerPheThiseryTrIpIeaIatRPvalArgGImet	40
Dd		119	TCTGTAAAGGGTTCTGGATCACGCTTTAACAGCATACGATCGGCTGGGTGGCCCAATG	178
Oy		41	ProGIlylsgIyleuGIlyrMerGIyleuIlleTyrrProGIyaSPserAspThrIlystYr	60
Dd		179	CCCCGAAAAGCCCTGGAGTGATGGGAGATCATCTATCCTGGTAGCTGTGATACCAGATAc	238
Oy		61	SerProSerPheGIingIylgInValThrlIeserylaspIysSerValSetThralatyR	80
Dd		239	AGCCCGTCCTTCCAAAGGCCAAGTCCACCATCTCAACCCACAAGTCCATCAGACCGCCCTAC	298
Oy		81	IeuGIlnTrpSerSertIeulyrProSerAspSerAlaValTyrrPheCyalaIdghIsasrp	100
Dd		299	CTGCAAGTGGACACCTGAAAGGCTCGGACACCCCATGTATTACTGTGCAGAAGC---	355
Oy		101	ValGIlyrCyssSerSerSerAsnCyalaIalysrTrProGIlyrPheGIlnHietRpIy	120
Dd		356	-----GSTAGCAGCAGCTGGTATCCAGCAAAAACTGATTCGACCCCTGGGGC	403
Oy		121	GIingIlyrIeuValThrValSerSer	129
Dd		404	CAGGGAAACCTGGTCAACCGTCTCTCA	430

ORGANISM

REFERENCE	1 (bases 1 to 1114)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Pacific Northwest National Laboratory

FEATURES

Plate: LLAM12781 row: g column: 22
High quality sequence stop: 736.

```

/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5750445"
/lab_host="DH10B"
/clone_id="NIH_MGC_122"
/notes="Organ: pooled lung and spleen; Vector: pCMV-Sport6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

```

ORIGIN

Alignment Scores:

Pred. No.:	3,35e-49	Length:	1114
Score:	524.00	Matches:	99
Percent Similarity:	84.6%	Conservative:	11
Best Local Similarity:	76.2%	Mismatches:	6
Query Match:	74.9%	Indels:	14
DB:	3	Gaps:	2

US-10-092-640-32 (1-129) x BM920470 (1-1114)

```

QY      1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysProGlyGlnSerLeuLysIle 20
       ::::::::::::::::::::
DB      126 GAGGTGCACCTGGTGCAGTCTGGAGCAGGTGAAAAACCCGGGAGTCTCTGAAGATC 185
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTyrValArgGlnMet 40
       186 TCCTGTAAAGGGTTCTGGATACAGCTTTACCACTACTGATCGGCTGGGTGGCCAGATG 245
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
       ::::::::::::::::::::
DB      246 CCCGGGAAAGGCTGTGAGTGGATGGGATCATCTATCTGTGACTCTGATACCAATAC 305
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
       ::::::::::::::::::::
DB      306 ACCCGGCTCTTCCAAAGGCCAGGTCAACCATCTCAAGCCGACAGTCCATCGACCGCTTAC 365
QY      81 LeuGlnTyrPheSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHis--- 99
       ::::::::::::::::::::
DB      366 CTGCAGTGGAGCAGCCTGGAAGGCTCGACACCGCATATTAATCTGTCGAGACATGTA 425
QY      100 AspValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGlyLysIleTyrPheGlnHisTyr 119
       426 GGGGCTGGA-----TTTGACTACTGG 446
DB      120 GlyGlnGlyThrLeuValThrValSerSer 129
       ::::::::::::::::::::
DB      447 GGGCAGGGAACCTGTGTCACTCTCTCTCA 476

RESULT 5
LOCUS   DA978565 SYN02 Homo sapiens cDNA clone SYN02009762 5', mRNA
DEFINITION DA978565 SYN02 Homo sapiens cDNA clone SYN02009762 5', mRNA
ACCESSION DA978565
VERSION   DA978565.1 GI:82439030
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
          Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Makaguri,H.,
          Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
          Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
          Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
          Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
          Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
          Genome Res. 16 (1), 55-65 (2006)
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology

```

FEATURES

Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

Location/Qualifiers

1..573

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="SYNOV2009762"

/tissue="synovial membrane tissue from rheumatoid arthritis"

/clone_lib="SYNOV2"

/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.:	1.51e-49	Length:	573
Score:	523.50	Matches:	98
Percent Similarity:	86.0%	Conservative:	13
Best Local Similarity:	76.0%	Mismatches:	15
Query Match:	74.8%	Indels:	3
DB:	9	Gaps:	1

US-10-092-640-32 (1-129) x DA978565 (1-573)

```

QY      1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysProGlyGlnSerLeuLysIle 20
       ::::::::::::::::::::
DB      114 GAGGTGCACCTGGTGCAGTCTGGAGCAGGTGAAAAACCCGGGAGTCTCTGAAGATC 173
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTyrValArgGlnMet 40
       174 TCCTGTAAAGGGTTCTGGATACAGCTTTACCACTACTGATCGGCTGGGTGGCCAGATG 233
DB      174 TCCTGTAAAGGGTTCTGGATACAGCTTTACCACTACTGATCGGCTGGGTGGCCAGATG 233
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
       ::::::::::::::::::::
DB      234 CCCGGGAAAGGCTGTGAGTGGATGGGATCATCTATCTGTGACTCTGATACCAATAC 293
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
       ::::::::::::::::::::
DB      294 AGCCGCTCTTCCAAAGGCCAGGTCAACCATCTCAAGCCGACACTCATCCACCGCTTAC 353
QY      81 LeuGlnTyrPheSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
       ::::::::::::::::::::
DB      354 CTGCAGTGGAGCAGCCTGGAAGGCTCGACACCGCATATTAATCTGTCGAGACTACT 413
QY      101 ValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGlyLysIleTyrPheGlnHisTyrGly 120
       414 CATGGGTATTACTATGATAGTAGTAGTCTTAT-----TACTATCTTGACTACTGGGGC 464
DB      121 GlnGlyThrLeuValThrValSerSer 129
       ::::::::::::::::::::
DB      465 CAGGGAACCTGTGTCACTCTCTCTCA 491

RESULT 6
LOCUS   BG685604 SYN01 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765028 5',
DEFINITION BG685604 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765028 5',
ACCESSION BG685604
VERSION   BG685604
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 795)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT

```

Email: c9abps-r@mail.nih.gov
 Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM623 row: d column: 21
 High quality sequence stop: 789.

FEATURES

source

```

1.795
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4765028"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

ORIGIN

Alignment Scores:

```

Pred. No.: 2,38e-49 Length: 795
Score: 523.50 Matches: 98
Percent Similarity: 86.0% Conservative: 13
Best Local Similarity: 76.0% Mismatches: 13
Query Match: 74.8% Indels: 5
DB: 2 Gaps: 2

```

US-10-092-640-32 (1-129) x BG685604 (1-795)

```

QY 1 GlnValGlnLeuGlnSerGlyAlaGluLeuLeuProGlyGlnSerLeuVal 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 94 GAGGTGACAGCTGGTGCAGTGTGAGCAGAGTGAAGCCCGGAGTCTCGAAGATC 153

QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
   TCCCTGTAAGAGGTTCTGGATACAGCTTACCACTACTGATCGGCTGGGCGCCAGATG 213
DB 154 TCCCTGTAAGAGGTTCTGGATACAGCTTACCACTACTGATCGGCTGGGCGCCAGATG 213

QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 214 CCCGGGAAAGGCTGAGTGGATGGGATCATCTATCTGCTGATCTAATACCAATAC 273

QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 274 AGCCGCTCTCCCAAGCCAGGTCATTATTTACGCCGACAGTCATCACTACCGCTAC 333

QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
   TCGCTATGAGAGGCTCGAAGGCTCGACACCGCATGATTAATGTCGAGACATGGT 393
DB 334 TCGCTATGAGAGGCTCGAAGGCTCGACACCGCATGATTAATGTCGAGACATGGT 393

QY 101 ValGlyTyrCysSerSerSerLeuValAlaLysTrpProGlyTyrPheGlnHisTrpGly 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 394 ---GGTTACTATGATTCGGGGAC-----CCGCACTAATGATTCCTCGGGC 438

QY 121 GlnGlyThrLeuValThrValSerSer 129
   |||||
DB 439 CAGGGAACTTACTGACCGTCTCTCA 465

```

RESULT 7
 BG754454 873 bp mRNA linear EST 15-MAY-2001
 LOCUS 602710060FL NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846527 5',
 DEFINITION mRNA sequence.

ACCESSION

BG754454
 BG754454.1 GI:14065094
 EST.
 KEYWORDS
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE

1 (bases 1 to 873)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: c9abps-r@mail.nih.gov
 Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM687 row: h column: 16
 High quality sequence stop: 821.

FEATURES

source

```

1.873
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4846527"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

ORIGIN

Alignment Scores:

```

Pred. No.: 2,72e-49 Length: 873
Score: 523.50 Matches: 98
Percent Similarity: 86.0% Conservative: 13
Best Local Similarity: 76.0% Mismatches: 13
Query Match: 74.8% Indels: 5
DB: 2 Gaps: 2

```

US-10-092-640-32 (1-129) x BG754454 (1-873)

```

QY 1 GlnValGlnLeuGlnSerGlyAlaGluLeuLeuProGlyGlnSerLeuVal 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 94 GAGGTGACAGCTGGTGCAGTGTGAGCAGAGTGAAGCCCGGAGTCTCGAAGATC 153

QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
   TCCCTGTAAGAGGTTCTGGATACAGCTTACCACTACTGATCGGCTGGGCGCCAGATG 213
DB 154 TCCCTGTAAGAGGTTCTGGATACAGCTTACCACTACTGATCGGCTGGGCGCCAGATG 213

QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 214 CCCGGGAAAGGCTGAGTGGATGGGATCATCTATCTGCTGATCTAATACCAATAC 273

QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 274 AGCCGCTCTCCCAAGCCAGGTCATTATTTACGCCGACAGTCATCACTACCGCTAC 333

QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
   TCGCTATGAGAGGCTCGAAGGCTCGACACCGCATGATTAATGTCGAGACATGGT 393
DB 334 TCGCTATGAGAGGCTCGAAGGCTCGACACCGCATGATTAATGTCGAGACATGGT 393

```


Score: 520.00 Matches: 97
 Percent Similarity: 84.5% Conservative: 12
 Best Local Similarity: 75.2% Mismatches: 10
 Query Match: 74.3% Indels: 10
 DB: 2 Gaps: 1

US-10-092-640-32 (1-129) x BG755575 (1-607)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
 DB 102 GAGGTCCAGCTGGTGTGAGTCTGGAGCAGAGTGAAGAAAGCCGGGAGTCTCTGAAGATC 161
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
 DB 162 TCTGTGAAGGCTTGTGATACACTTACAGCTACGATCGGCTGGGTCGCGCAGATG 221
 QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
 DB 222 CCGGGAAAGCCTGGAGTGGATGGGATCATCTATCTGTGACTGTGATACCAATAC 281
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 282 AGCCCTCTCTCCAGGCGCAGTCCACCATCTCAGCCGACCAAGTCACATCAGACCGCCTAC 341
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 DB 342 CTGCACGTGAGCAGCCTGGAAGGCTCGGACACCGCATGTATTACTGTGGCTCCACTCA 401
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHisTyrGly 120
 DB 402 ACGGCTCTGCTGCTCT-----TTTGATATCTGGGCG 411
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 DB 432 CAAGGACAATGGTCAACCGTCTCTCA 458

RESULT 10
 DA988827 568 bp mRNA linear EST 09-NOV-2005

LOCUS DA988827 SYN0V3 Homo sapiens cDNA clone SYN0V3000537 5', mRNA
 DEFINITION sequence.

ACCESSION DA988827
 VERSION DA988827.1 GI:81266627

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 568)
 Kimura, K., Wakematsu, A., Suzuki, Y., Oca, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsutsumi, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Rie, R., Kuahida, N.,
 Yonekawa, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Magatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanabe, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

JOURNAL PUBMED 16344560

COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction;
 Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one

FEATURES pass sequencing: RAB.
 Location/Qualifiers
 source 1..568
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SYNOV3000537"
 /tissue_type="synovial membrane tissue from rheumatoid
 arthritis"
 /clone_lib="SYNOV3"
 /note="Vector: pME18SFLJ3"

ORIGIN

Alignment Scores:
 Pred. No.: 9,49e-49 Length: 568
 Score: 516.50 Matches: 98
 Percent Similarity: 84.5% Conservative: 11
 Best Local Similarity: 76.0% Mismatches: 13
 Query Match: 73.8% Indels: 7
 DB: 9 Gaps: 2

US-10-092-640-32 (1-129) x DA988827 (1-568)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
 DB 115 GAGGTCCAGCTGGTGTGAGTCTGGAGCAGAGTGAAGAAAGCCGGGAGTCTCTGAAGATC 174
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
 DB 175 TCTGTGAAGGCTTGTGATACACTTACAGCTACGATCGGCTGGGTCGCGCAGATG 234
 QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
 DB 235 CCGGGAAAGCCTGGAGTGGATGGGATCATCTATCTGTGACTGTGATACCAATAC 294
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 295 AGCCCTCTCTCCAGGCGCAGTCCACCATCTCAGCCGACCAAGTCACATCAGACCGCCTAC 354
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 DB 355 CTGCACGTGAGCAGCCTGGAAGGCTCGGACACCGCATGTATTACTGTGGCTCCACTCA 414
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHisTyrGly 120
 DB 415 GCGAGCTAC-----TACCCGTGGCTGCT---TTTGATATCTGGGCG 453
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 DB 454 CAAGGACAATGGTCAACCGTCTCTCA 480

RESULT 11 875 bp mRNA linear EST 16-JUN-2002

LOCUS BO711293 875 bp mRNA linear EST 16-JUN-2002
 DEFINITION AGENCOURT_8349985 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280207
 5', mRNA sequence.

ACCESSION BO711293
 VERSION BO711293.1 GI:21850192

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 875)
 NIH-MGC http://imgc.nhl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE NIH-MGC http://imgc.nhl.nih.gov/
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM2471 row: a column: 08
 High quality sequence stop: 594.

FEATURES

source

```

1.875
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6280207"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

```

ORIGIN

Alignment Scores:

Pred. No.:	2,276-48	Length:	875
Score:	515.50	Matches:	97
Percent Similarity:	85.3%	Conservative:	13
Best Local Similarity:	75.2%	Mismatches:	12
Query Match:	73.6%	Indels:	7
DB:	3	Gaps:	1

US-10-092-640-32 (1-129) x B0711293 (1-875)

```

QY      1  GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      85  GAGGTGACAGCTGATGAGTCTGAGCAGAGGTGAAAAAGCCGGGGAGTCTCGAAGATC 144

QY      21  SerCyblybGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValaArgGlnMet 40
      |||||||
DB      145  TCCTGTAAAGGGTTCTGGATACAGTTTACAGTCACTGATCGGGGTGGCCAGATG 204

QY      41  ProGlyLysGlyLeuGlnLutyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
      |||||||
DB      205  CCCGGGAAAGCCCTGGAGTGGATGGGATCATCTATCTCGGACTCTATACGACATTC 264

QY      61  SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      |||||||
DB      265  AGCCCGTCTCTCCAAAGGCCAGGTACCATCTCAGTCGACCAAGTCCATACCCGCTAC 324

QY      81  LeuGlnTyrPseSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
      |||||||
DB      335  CTGGAGTGGAGCGAGTCTGAAGGCTCTGGACACCGCATGTATTATTGTCCGAGACAT--- 381

QY      101  ValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGlyLutyrPheGlnHisTyrGly 120
      |||||||
DB      382  -----CTCAGACTGCTACTCAACTCAACCTTTTACCACTGGGCG 423

QY      121  GlnGlyThrLeuValThrValSerSer 129
      |||||||
DB      424  CAGGGAAACCTGGTCACTCTCTCTCA 450

RESULT 12
DA981607  DA981607  573 bp  mRNA  linear  EST 13-NOV-2005
LOCUS      DA981607  SYN0V2 Homo sapiens cDNA clone SYN0V2013648 5', mRNA
DEFINITION sequence.
ACCESSION  DA981607
VERSION     DA981607.1  GI:823444094
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE

1 (bases 1 to 573)

AUTHORS

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Teuriltan,K., Wakaquri,H.,
 Ishi,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Magatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Takao Isogai
 FUJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@flj.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.
 Location/Qualifiers

FEATURES

source

```

1.573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SYNOV2013648"
/tissue_type="synovial membrane tissue from rheumatoid
arthritis"
/clone_lib="SYNOV2"
/note="Vector: pME18SFL3"

```

ORIGIN

Alignment Scores:

Pred. No.:	1,436-48	Length:	573
Score:	515.00	Matches:	95
Percent Similarity:	84.5%	Conservative:	14
Best Local Similarity:	73.6%	Mismatches:	10
Query Match:	73.6%	Indels:	10
DB:	9	Gaps:	1

US-10-092-640-32 (1-129) x DA981607 (1-573)

```

QY      1  GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      116  GAGGTGACAGCTGATGAGTCTGAGCAGAGGTGAAAAAGCCGGGGAGTCTCGAAGATC 175

QY      21  SerCyblybGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValaArgGlnMet 40
      |||||||
DB      176  TCCTGTAAAGGGTTCTGGATACAGTTTACAGTCACTGATCGGGGTGGCCAGATG 235

QY      41  ProGlyLysGlyLeuGlnLutyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
      |||||||
DB      236  CCCGGGAAAGCCCTGGAGTGGATGGGATCGCTATCTCGGACTCTGAGACCAAGATTC 295

QY      61  SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      |||||||
DB      296  AGTCCGCTCTCTCCAAAGGCCAGGTACCATTTTACGCCGACCAACATCGTACCGCTTAC 355

QY      81  LeuGlnTyrPseSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
      |||||||
DB      356  CTGGAGTGGAGCGAGCTCTGAAGGCTCTGGACACCGCATGTATTATTCTGCGCAGATCGACA 415

QY      101  ValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGlyLutyrPheGlnHisTyrGly 120
      |||||||
DB      416  GATGGCTACAGTATGAGG-----GACTACTGGGCG 445

```


Qy 121 GlnGlyThrLeuValThrValSerSer 129
 |||||
 Db 446 CAGGGAACTCTGATCACCCTCTCTCA 472

RESULT 13
 DB190036
 LOCUS DB190036 TLUNG2 Homo sapiens cdna clone TLUNG2000849 5', mRNA
 DEFINITION DB190036 TLUNG2 Homo sapiens cdna clone TLUNG2000849 5', mRNA
 sequence.
 DB190036 DB190036 GI:83552147
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 530)

REFERENCE
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

JOURNAL
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.

FEATURES
 source 1..530
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TLUNG2000849"
 /tissue_type="lung, tumor tissue"
 /clone_id="TLUNG2"
 /note="Vector: pME18SFL3"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,466-48 Length: 530
 Score: 514.50 Matches: 98
 Percent Similarity: 86.2% Conservative: 14
 Best Local Similarity: 75.4% Mismatches: 11
 Query Match: 73.5% Indels: 7
 DB: 9 Gaps: 3

US-10-092-640-32 (1-129) x DB190036 (1-530)

Db 236 CCGGGAAGAGCCTGGAGTGATGGGATCATCTATCTCTGTGATACAGTAT 295
 Qy 61 SerProSerPheGlnGlyGlnValThrIleSerValAspIleSerValSerThrAlaTyr 80
 |||||
 Db 296 AGTCCGTTCTTCCAAAGCCAGGTGATCATCTAGTCAGACAAATCATCACACCGCTTCA 355

Qy 81 LeuGlnThrSerSerLeuIleuysProSerAspSerAlaValTyrPheCysAlaArg---His 99
 |||||
 Db 356 CTGCAGTGGAGTGGCTGGAGCCCTGGACAGCGCCATGATTACTGTGGAGACTTTCA 415

Qy 100 AspValGlyTyrCysSerSerSerAsnCyAlaIleTyrProGluTyrPheGlnHisTyr 119
 |||||
 Db 416 TCCTTAGCGTATGCAACAC-----TGG---TACTTCTTTGACTACTGG 457

Qy 120 GlyGlnGlyThrLeuValThrValSerSer 129
 |||||
 Db 458 GGCAGGAAACCTGTGGCCACCGTCTCTCA 487

RESULT 14
 DA969213
 LOCUS DA969213 STOMA2 Homo sapiens cdna clone STOMA2008143 5', mRNA
 DEFINITION DA969213 STOMA2 Homo sapiens cdna clone STOMA2008143 5', mRNA
 sequence.
 DA969213 DA969213 GI:82348271
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 584)

REFERENCE
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

JOURNAL
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.

FEATURES
 source 1..584
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="STOMA2008143"
 /tissue_type="stomach"
 /clone_id="STOMA2"
 /note="Vector: pME18SFL3"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,686-48 Length: 584
 Score: 514.50 Matches: 99
 Percent Similarity: 86.2% Conservative: 13
 Best Local Similarity: 76.2% Mismatches: 15
 Query Match: 73.5% Indels: 3

DB: 9 Gaps: 2

US-10-092-640-32 (1-129) x DA969213 (1-584)

QY 1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysProGlyGlySerLeuLysIle 20
:::|||||

DB 105 GAGGTGCAGCTGCTGACAGTCTGACAGCTGAAAGCCCGGAGCTCTGAAGATC 164

QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
:::|||||

DB 165 TCCTGTAAAGGCTCTGAGATTTCAGTTTACCAACACCGGATGCTCGGATCCGCAAGATG 224

QY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
|||||

DB 225 CCGGGGAAAGGCTGGAGCTATAGGGAGCACTATCTTGTGACTGTGATCCAGATAT 284

QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
:::|||||

DB 285 AACCGTCATTCCAAAGGCCAGGTCACATCTCAGTCGACAAAGTCCATCCACCGCTAT 344

QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg---His 99
:::|||||

DB 345 CTACAGGTGACAGCCTGAAAGCCTCGGACACCGCGCTCTATTACTGTGCGGATTAGAG 404

QY 100 AspValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLysPheGlnHisTrp 119
405 AGCTTGGATTTAGTCTGATGACCAATTCCTCTCC-----AGCGCTTGATGTCTGG 458

QY 120 GlyGlnGlyThrLeuValThrValSerSer 129
459 GGCCAAGGAACAATGTCTACCGTCTCTTCA 488

DB

RESULT 15

BF663762 862 bp mRNA linear EST 21-DEC-2000

LOCUS 602145490F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4308838 5',

DEFINITION mRNA sequence.

ACCESSION BF663762.1 GI:11937657

VERSION BF663762.1 GI:11937657

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 862)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Louis W. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>

Plate: L1CM181 row: d column: 23

High quality sequence stop: 715.

Location/Qualifiers

1. 862

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4308838"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_48"

/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	4,31e-48	Length:	862
Score:	513.00	Matches:	100
Percent Similarity:	86.2%	Conservative:	12
Best Local Similarity:	76.9%	Mismatches:	7
Query Match:	73.3%	Indels:	7
DB:	7	Gaps:	2

US-10-092-640-32 (1-129) x BF663762 (1-862)

QY 1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysProGlyGlySerLeuLysIle 20
:::|||||

DB 90 GAGGTGCAGCTGCTGACAGTCTGACAGGAGGAAAGCCCGGAGCTCTGAAGATC 149

QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
:::|||||

DB 150 TCCTGTAAAGGCTCTGAGTTACAGCTTACCACTGATCGGCTGGGTGCGCAGATG 209

QY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
|||||

DB 210 CCGGGGAAAGGCTGGAGTGGAGTGGAGTCACTATCTCGGAGCTGATCCAGATAC 269

QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
:::|||||

DB 270 AGCCGCTTTCACAGGCCAGGTCACATCTCAGCGCAAGTCCATCAGCACCGGCTAC 329

QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg---His 99
:::|||||

DB 330 CTGACGTGAGAGAGCCTGAAAGCCTCGGACACCGCATGTATTACTGTGCGAGACGGGT 389

QY 100 AspValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLysPheGlnHisTrp 119
|||||

DB 390 CACACTGGGTATTGATGATGCTGTGCTGC-----TACGAGCCTACTGG 434

QY 120 GlyGlnGlyThrLeuValThrValSerSer 129
|||||

DB 435 GGCCA-GGAACCTGCTACCGTCTCTCTCA 463

Search completed: May 25, 2006, 21:12:28

Job time : 4245.95 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 17:06:37 ; Search time 167.7 Seconds
(without alignments)
2158.972 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700
Sequence: 1 QVQLQSGAELEKKGESLKI.....AKRPEYFGHGGCTLVTVSS 129

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWB.spool/US10092640/runat_25052006.155719.5922/app.query.fasta_1
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humand0.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-NODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abs02h -USER=US10092640@CGN 1.1.252@runat_25052006.155719.5922
-NCPU=6 -ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents_NA: *
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq: *
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq: *
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq: *
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq: *
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq: *
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq: *
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCUTS_COMB.seq: *
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq: *
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq: *
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	700	100.0	774	2	US-08-665-202-4
2	700	100.0	774	3	US-09-315-574-4
3	520	74.3	462	3	US-09-042-353-359
4	520	74.3	462	3	US-08-758-417A-207
5	510.5	72.9	361	3	US-09-025-769B-66
6	510.5	72.9	361	3	US-09-490-070A-66
7	510.5	72.9	361	3	US-09-490-153-66
8	510.5	72.9	361	3	US-09-490-324-66

9	500	71.4	414	3	US-09-042-353-353	Sequence 353, App
10	500	71.4	414	3	US-08-758-417A-201	Sequence 201, App
11	486	69.4	421	3	US-09-905-243-6	Sequence 6, App1
12	483	69.0	700	3	US-08-545-809A-51	Sequence 51, App1
13	483	69.0	700	3	US-09-515-697-51	Sequence 51, App1
14	465.5	66.5	383	2	US-08-053-131-176	Sequence 176, App
15	465.5	66.5	383	2	US-08-096-762-176	Sequence 176, App
16	460.5	65.8	357	2	US-08-053-131-156	Sequence 156, App
17	460.5	65.8	357	2	US-08-096-762-156	Sequence 156, App
18	460.5	65.8	351	2	US-08-053-131-177	Sequence 177, App
19	460.5	65.8	351	2	US-08-096-762-177	Sequence 177, App
20	460.5	65.7	362	2	US-08-053-131-170	Sequence 170, App
21	460	65.7	362	2	US-08-096-762-170	Sequence 170, App
22	459.5	65.6	417	3	US-09-905-243-39	Sequence 39, App1
23	458	65.4	348	2	US-08-053-131-157	Sequence 157, App
24	458	65.4	348	2	US-08-096-762-157	Sequence 157, App
25	457	65.3	326	2	US-08-053-131-167	Sequence 167, App
26	457	65.3	326	2	US-08-096-762-167	Sequence 167, App
27	457	65.3	366	2	US-08-053-131-163	Sequence 163, App
28	457	65.3	366	2	US-08-096-762-163	Sequence 163, App
29	457	65.3	477	3	US-08-724-752-16	Sequence 16, App1
30	457	65.3	477	3	US-09-614-092A-16	Sequence 16, App1
31	454	64.9	348	2	US-08-053-131-160	Sequence 160, App
32	454	64.9	348	2	US-08-096-762-160	Sequence 160, App
33	452	64.6	358	2	US-08-053-131-172	Sequence 172, App
34	452	64.6	358	2	US-08-096-762-172	Sequence 172, App
35	452	64.6	360	2	US-08-053-131-161	Sequence 161, App
36	452	64.6	360	2	US-08-096-762-161	Sequence 161, App
37	451	64.4	349	2	US-08-053-131-165	Sequence 165, App
38	451	64.4	349	2	US-08-096-762-165	Sequence 165, App
39	450.5	64.4	384	2	US-08-053-131-168	Sequence 168, App
40	450.5	64.4	384	2	US-08-096-762-168	Sequence 168, App
41	450	64.3	297	3	US-09-042-353-91	Sequence 91, App1
42	450	64.3	297	3	US-08-758-417A-355	Sequence 355, App
43	448.5	64.1	312	3	US-09-042-353-123	Sequence 123, App
44	448.5	64.1	312	3	US-08-758-417A-387	Sequence 387, App
45	448.5	64.1	325	2	US-08-053-131-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-08-665-202-4
Sequence 4, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

```
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION:
OTHER INFORMATION: antibody C6.5"
US-08-665-202-4

Alignment Scores:
Pred. No.: 3,52e-75 Length: 774
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-092-640-32 (1-129) x US-08-665-202-4 (1-774)
QY 1 GlnValGlnLeuLengInserGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
Db 1 CAGGGTGCACCTGTTGCAAGTCTGGGGCAGAGTTGAAAAAACCAGGGAGTCTTGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 TCTGTGAAGGGTTCTGGATACAGCTTTACAGCTACTGGATGCGCGGGTGGCCGAGATG 120
QY 41 ProGlyLysGlyLeuGluLutyrMetGlyLeuLleTyrProGlyLysSerAspThrLysTyr 60
Db 121 CCGGGGAAAGGCGCTGAGTACATGGGGCTCATCTATCTCGTGACTGTACACCAATATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 ACCCGCTCTTCCAAAGGCCAGGTCACCAATCTCATGTGACAAGTCCGTCAGCACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 TTGCATATGAGCAGCTCTGAAGCCCTCGACAGCGCGCTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLutyrPheGlnHisTrpGly 120
Db 301 GGGGGATATTGCAAGTATCCAACTCCGCAAGTGGCTGAATATCTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
Db 361 CAGGGCACCCCTGTGTCACCGTCTCTCTCA 387

RESULT 2
US-09-315-574-4
Sequence 4, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Huse P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
```

```
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION:
OTHER INFORMATION: antibody C6.5"
US-09-315-574-4

Alignment Scores:
Pred. No.: 3,52e-75 Length: 774
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-32 (1-129) x US-09-315-574-4 (1-774)
QY 1 GlnValGlnLeuLengInserGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20
Db 1 CAGGTGCAGCTGTTGCAAGTCTGGGGCAGAGTTGAAAAAACCAGGGAGTCTTGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 TCTGTGAAGGGTTCTGGATACAGCTTTACAGCTACTGGATGCGCGGGTGGCCGAGATG 120
QY 41 ProGlyLysGlyLeuGluLutyrMetGlyLeuLleTyrProGlyLysSerAspThrLysTyr 60
Db 121 CCGGGGAAAGGCGCTGAGTACATGGGGCTCATCTCGTGACTGTACACCAATATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 ACCCGCTCTTCCAAAGGCCAGGTCACCAATCTCATGTGACAAGTCCGTCAGCACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 TTGCATATGAGCAGTCTGAAGCCCTCGACAGCGCGCTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLutyrPheGlnHisTrpGly 120
```

Db 301 GTGGATATGCGAGTACTTCCAACTGCGCAAGGCGCTCAATCTTCAGCATGGGCG 360
Qy 121 GInGlyThrluValThrlValSerSer 129
Db 361 CAGGGACCTGGTGGTCAACGCTCTCTCA 387

RESULT 3
US-09-042-353-359
Sequence 359, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
CURRANT APPLICATION DATA: Patent Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-359

Alignment Scores:
Pred. No.: 9.8e-54 Length: 462
Score: 520.00 Matches: 97
Percent Similarity: 83.7% Conservative: 11
Best Local Similarity: 75.2% Mismatches: 9
Query Match: 74.3% Indels: 12
DB: 3 Gaps: 1

US-10-092-640-32 (1-129) x US-09-042-353-359 (1-462)

Qy 1 GlnValGlnLeuLeuGlnSerGlyValGluLeuLysProGlyGluSerLeuLysIle 20
Db 58 GAGTGCAGCTGAGTGCAGTGTGAGCAGAGGTAAGCCCGGAGGTCTTGAGATC 117
Qy 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTyrValArgGlnMet 40
Db 118 TCCTGTAAAGGTTCTGATACAGCTTACCGGCTACGTGATCGGCTGGGCGCCAGATG 177
Qy 41 ProGlyLysGlyLeuGluLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 178 CCGGGAAAGGCTGGAGTGGATGGGATCATCTTACCTGTGACTGTATACCATAC 237
Qy 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 238 AGCCGCTCTTCCAGGCCAGGTACCAATCTCAGCCGACAGTCCATCAGACCCGCTAC 237
Qy 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 298 CTGCAGTGGAGAGCGCTGAAGGCGCTCGACACCGCATGATATCTGTGGAGAGACAA 357
Qy 101 ValGlyTyrCysSerSerSerSerCysAlaLysTyrProGluLysPheGlnHisTyrGly 120
Db 358 CTGGGC-----CTCTTGACTACTGGGC 381

Db 121 GInGlyThrluValThrlValSerSer 129
Db 382 CAGGGACCTGGTGGTCAACGCTCTCTCA 408

RESULT 4
US-08-758-417A-207
Sequence 207, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 207:
US-08-758-417A-207
Alignment Scores:
Pred. No.: 9.8e-54 Length: 462
Score: 520.00 Matches: 97
Percent Similarity: 83.7% Conservative: 11
Best Local Similarity: 75.2% Mismatches: 9
Query Match: 74.3% Indels: 12
DB: 3 Gaps: 1
US-10-092-640-32 (1-129) x US-08-758-417A-207 (1-462)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGlnSerLeuLysIle 20
DB 58 GAGGTGACCTGCTGAGTCTGTGAGCAGAGGTGAAAAGCCCGGGGAGTCTGTGAAGATC 117
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaIleArgValArgGlnMet 40
DB 118 TCCTGTAAAGGGTTCGTGATACAGCTTACCGGCTACTGATCGGCTGGGTGGCCAGATG 177
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60

DB 178 CCGGGAAAGCCTGAGATGAGTGGGATCATCTACTCTGAGTACTGTATACACATAC 237
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 238 AGCCGCTCTTCCAGAGCCAGAGTCCATCTCAGCCAGCAAGTCCATCAGCAGCCCTTAC 297
QY 81 LeuGlnTyrPseSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 298 CTGCACTGAGCAGCCTTAAGGCTTCGACACCGCCATGTATTACTGTGCGAGAACCA 357
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHisTrpGly 120
DB 358 CTGGCC-----CTTTGACTACTGGGGC 381
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 382 CAGGAAACCTGGTCCAGCTCTCTCA 408
RESULT 5
US-09-025-769B-66
Sequence 66, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic gene"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..360
OTHER INFORMATION: /product= "VHS"
US-09-025-769B-66
Alignment Scores:
Pred. No.: 9.75e-53 Length: 361
Score: 510.50 Matches: 98

Percent Similarity: 83.2% Conservative: 11
 Best Local Similarity: 74.8% Mismatches: 9
 Query Match: 72.9% Indels: 13
 DB: 3 Gaps: 2

US-10-092-640-32 (1-129) x US-09-025-769B-66 (1-361)

```

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
       1 GAAGTGCATTTGGTTTCAGACGGCGCGAAGTGAATAAACCGGCGCAAACTGAAATTT 60
DB      21 SerCysIleGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
       61 AGCTGCAGAGGTTCCCGATTTCTTTACAGCTATTGGATTGGCTGGGTCGCGCAGATG 120
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
       121 CTGGGAAGGGTCTCGAGTGGATGGGCTATTATTCGGGCGATAGCGATACCCGTTAT 180
DB      61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
       181 TCTCCAGCTTTTCAGGCGCAGGTGACCATTTAGCGCGATTAAGCATTTACACCGCTAT 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
       241 CTTCAATGAGACGAGCTGAAAGCGAGCATACGCCATGTATTATTCGCGCGCTTGGGCG 300
QY      99 HisAspValGlyTyrCysSerSerSerAsnCyAlaLysTrpProGlnTyrPheGlnHis 118
       301 GGGGATGGCTTTATATCG-----ATGAGATTAT 327
DB      119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
       328 TGGGGCCAAGGACCCCTGTGACGTTAGCTCA 360

```

RESULT 6

US-09-490-070A-66

Sequence 66, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ilag, Vic

Ge, Liming

Moreney, Simon

Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McAnuliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 361 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic gene"

FEATURE:

NAME/KEY: CDS

LOCATION: 1..360

OTHER INFORMATION: /product= "VHS"

SEQUENCE DESCRIPTION: SEQ ID NO: 66:

US-09-490-070A-66

Alignment Scores: Pred. No.: 9 75e-53 Length: 361

Score: 510.50 Matches: 98

Percent Similarity: 83.2% Conservative: 11

Best Local Similarity: 74.8% Mismatches: 9

Query Match: 72.9% Indels: 13

DB: 3 Gaps: 2

US-10-092-640-32 (1-129) x US-09-490-070A-66 (1-361)

```

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
       1 GAAGTGCATTTGGTTTCAGACGGCGCGAAGTGAATAAACCGGCGCAAACTGAAATTT 60
DB      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
       61 AGCTGCAGAGGTTCCCGATTTCTTTACAGCTATTGGATTGGCTGGGTCGCGCAGATG 120
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
       121 CTGGGAAGGGTCTCGAGTGGATGGGCTATTATTCGGGCGATAGCGATACCCGTTAT 180
DB      61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
       181 TCTCCAGCTTTTCAGGCGCAGGTGACCATTTAGCGCGATTAAGCATTTACACCGCTAT 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
       241 CTTCAATGAGACGAGCTGAAAGCGAGCATACGCCATGTATTATTCGCGCGCTTGGGCG 300
QY      99 HisAspValGlyTyrCysSerSerSerAsnCyAlaLysTrpProGlnTyrPheGlnHis 118
       301 GGGGATGGCTTTATATCG-----ATGAGATTAT 327
DB      119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
       328 TGGGGCCAAGGACCCCTGTGACGTTAGCTCA 360

```

RESULT 7

US-09-490-153-66

Sequence 66, Application US/09490153

Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ilag, Vic

Ge, Liming

Moreney, Simon

Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

```

      ZIP: 10021
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/490,153
      FILING DATE: 24-Jan-2000
      PRIORITY APPLICATION DATA:
      APPLICATION NUMBER: US/09/025,769B
      FILING DATE: 18-FEB-1998
      APPLICATION NUMBER: EP 95 11 3021.0
      FILING DATE: 18-AUG-1995
      ATTORNEY/AGENT INFORMATION:
      NAME: James F. Haley, Jr., Esq.
      REGISTRATION NUMBER: 27,794
      REFERENCE/DOCKET NUMBER: MORPHO/5
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212)596-9000
      TELEFAX: (212)596-9090
      INFORMATION FOR SEQ ID NO: 66:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 361 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
      DESCRIPTION: /desc = "synthetic gene"
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..360
      OTHER INFORMATION: /product= "VH5"
      SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-490-153-66
Alignment Scores:
Pred. No.: 9,75e-53 Length: 361
Score: 510.50 Matches: 98
Percent Similarity: 83.2% Conservative: 11
Best Local Similarity: 74.8% Mismatches: 9
Query Match: 72.9% Indels: 13
DB: 3 Gaps: 2
US-10-092-640-32 (1-129) x US-09-490-153-66 (1-361)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGlnSerLeuLysIle 20
   ::::::::::::::::::::
DB 1 GAAGTGCATTGCTTCAGAGCGCGCGGAAGTGAACCAACCGGCGAAGCCTGAAATTT 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
   ::::::::::::::::::::
DB 61 AGCTGCAAGAGTTCCGGATATTCCTTTACGAGCTATGTGATTGGCTGGGTGCGCAGATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrIleTyr 60
   ::::::::::::::::::::
DB 121 CCTGGGAAGGCTCGAGTGCATGATTTATTCGCGGCGATGCGATACCGCTTAT 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
   ::::::::::::::::::::
DB 181 TCTCCGAGCTTCAGGCGCAGGTGACCATTTAGCGCGCATMAAAGCATTTAGCACCGCGTAT 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
   ::::::::::::::::::::
DB 241 CTTCAATGAGAGCCTGGAAGCGAGCGATACGCCCATATATTATTTGCGCGCTTGGGGC 300
QY 99 HisAspValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHis 118
   ::::::::::::::::::::
DB 301 GCGCATGCGTTTATATCG-----ATGATTTAT 327
QY 119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
   ::::::::::::::::::::
DB 328 TGGGGCCAAAGGACCCCTGGTGAACGTTAAGCTCA 360

```

```

      RESULT 8
      US-09-490-324-66
      Sequence 66, Application US/09490324
      Patent No. 6828422
      GENERAL INFORMATION:
      APPLICANT: Knappik, Achim
      Pack, Peter
      Ilag, Vic
      Ge, Liming
      Moroney, Simon
      Plueckhuhn, Andreas
      TITLE OF INVENTION: Protein/(poly)peptide libraries
      NUMBER OF SEQUENCES: 373
      CORRESPONDENCE ADDRESSES:
      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
      STREET: 1251 Avenue of the Americas
      CITY: New York
      STATE: New York
      COUNTRY: USA
      ZIP: 10021
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/490,324
      FILING DATE: 24-Jan-2000
      PRIORITY APPLICATION DATA:
      APPLICATION NUMBER: US/09/025,769
      FILING DATE: 18-FEB-1998
      APPLICATION NUMBER: EP 95 11 3021.0
      FILING DATE: 18-AUG-1995
      ATTORNEY/AGENT INFORMATION:
      NAME: James F. Haley, Jr., Esq.
      REGISTRATION NUMBER: 27,794
      REFERENCE/DOCKET NUMBER: MORPHO/5
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212)596-9000
      TELEFAX: (212)596-9090
      INFORMATION FOR SEQ ID NO: 66:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 361 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: other nucleic acid
      DESCRIPTION: /desc = "synthetic gene"
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..360
      OTHER INFORMATION: /product= "VH5"
      SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-490-324-66
Alignment Scores:
Pred. No.: 9,75e-53 Length: 361
Score: 510.50 Matches: 98
Percent Similarity: 83.2% Conservative: 11
Best Local Similarity: 74.8% Mismatches: 9
Query Match: 72.9% Indels: 13
DB: 3 Gaps: 2
US-10-092-640-32 (1-129) x US-09-490-324-66 (1-361)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGlnSerLeuLysIle 20
   ::::::::::::::::::::
DB 1 GAAGTGCATTGCTTCAGAGCGCGCGGAAGTGAACCAACCGGCGAAGCCTGAAATTT 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
   ::::::::::::::::::::
DB 61 AGCTGCAAGAGTTCCGGATATTCCTTTACGAGCTATGTGATTGGCTGGGTGCGCAGATG 120

```


QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 121 CCGGAGAGGCTCTCGAGTGAGTGGGATTAATTATCCGGGCATAGCCGTTAT 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 TCTCCAGCTTTAGGAGCCGAGTGACCTTAGCGCGGATTAAGCATTTAGCACCCTAT 240
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg----- 98
Db 241 CTTCATGAGCAGCCTGGAAGGAGGATACGCGCATGATATTATGCGCGCTTGGGGC 300
QY 99 HisAspValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGlyTyrPheGlnHis 118
Db 301 GCGGATGGCTTTATTCG-----ATGATTTAT 327
QY 119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
Db 328 TGGGGCCAAAGCACCTCTGTGACGTTAGCTCA 360
RESULT 9
US-09-042-353-353
Sequence 353, Application US/09042353
Patent No. 6255456
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699

FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 353:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-353
Alignment Scores:
Pred. No.: 2.2e-51 Length: 414
Score: 500.00 Matches: 94
Percent Similarity: 84.1% Conservative: 12
Best Local Similarity: 74.6% Mismatches: 10
Query Match: 71.4% Indels: 10
Gaps: 1
US-10-092-640-32 (1-129) x US-09-042-353-353 (1-414)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyxGlnSerLeuLysIle 20
Db 67 GAGGTGACACTGTGACAGTCTGAGCAGAGTGAAGAAAGCCGGGAGTCTCTGAAGATC 126
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTyrValArgGlnMet 40
Db 127 TCTGTAAAGGTTTCGATACAGCTTTACCACTTACTGATCCCTGGGTGCCCGAGATC 186
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 187 CCGGAGAAAGCCTGAGAGTGGGATGCATCGATCTGAGACTGTGATACCAAGATAC 246
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 247 AACCCGCTCTTCCAAAGCCAGGTCACATCTCAGCCGACAAGTCATCAGTACCGCTTAT 306
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 307 TTGCAATGAGCAGCCTGGAAGGCTTCGACACCGCATGATTAATCTGCGAGACA--- 363
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGlyTyrPheGlnHisTrpGly 120
Db 364 -----GCAACTGGAAGTGTACTTCTCTCTGGGC 396
QY 121 GlnGlyThrLeuValThr 126

```

Db
397 CGTGGACCTGCTACT 414
:::|||||
RESULT 10
US-08-758-417A-201
: Sequence 201, Application US/08758417A
: Patent No. 6300129
: GENERAL INFORMATION:
: APPLICANT: Lomborg, Nils
: Kay, Robert M.
: TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
: Producing Heterologous Antibodies
: NUMBER OF SEQUENCES: 417
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/758,417A
: FILING DATE: 02-Dec-1996
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/728,463
: FILING DATE: 10-OCT-1996
: APPLICATION NUMBER: US 08/544,404
: FILING DATE: 10-OCT-1995
: APPLICATION NUMBER: US 08/352,322
: FILING DATE: 07-DEC-1994
: APPLICATION NUMBER: US 08/209,741
: FILING DATE: 09-MAR-1994
: APPLICATION NUMBER: US 08/165,699
: FILING DATE: 10-DEC-1993
: APPLICATION NUMBER: US 08/161,739
: FILING DATE: 03-DEC-1993
: APPLICATION NUMBER: US 08/155,301
: FILING DATE: 18-NOV-1993
: APPLICATION NUMBER: US 08/096,762
: FILING DATE: 22-JUL-1993
: APPLICATION NUMBER: US 08/053,131
: FILING DATE: 26-APR-1993
: APPLICATION NUMBER: US 07/990,860
: FILING DATE: 16-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Serafini, Andrew T.
: REGISTRATION NUMBER: 41,303
: REFERENCE/DOCKET NUMBER: 01643-009030US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 201:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 414 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-08-758-417A-201
Alignment Scores:
Pred. No.: 2.2e-51 Length: 414
Score: 500.00 Matches: 94
Percent Similarity: 84.1% Conservative: 12
Best Local Similarity: 74.6% Mismatches: 10
Query Match: 71.4% Indels: 10

```

DB:	3	Gaps:	1
US-10-092-640-32 (1-129) x US-08-758-417A-201 (1-414)			
QY	1 GlnValGlnLeuLeuGlnSerGlyValaGluLeuLysProGlyGluSerLeuLysIle	20	
Db	67 GAAGTGCACCTGCTGATGACGTCTGGACCAAGGTAAGAAAGCCCGGGAGTCTTGAAATC	126	
QY	21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet	40	
Db	127 TCTGTGAAGGGTTCGATACAGCTTTCACGATTAAGTGGATGCGCTGGAGTCCCAATG	166	
QY	41 ProGlyLysGlyLeuGlnLysIleMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr	60	
Db	187 CCGGGAAGAGCCTGGAGATGGATGGAGATCATCTGCTGACTCTGATACCAAGATAC	246	
QY	61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr	80	
Db	247 AACCCCTCTTCCCAAGGCCAGGTCAACATCTGACCGCAAGTCCATCAGTACGCGCTAT	306	
QY	81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp	100	
Db	307 TTGCAATGAGAGAGCCTGAAGGCTCGGACACCGCATATGATCTGCGAAGCA---	363	
QY	101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHisTrpGly	120	
Db	364 -----CCGAACGTGGAACTGGTACTTCGTTCTCTGGGGC	396	
QY	121 GlnGlyThrLeuValThr 126		
Db	397 CGTGCACCTGTGCTACT 414		
RESULT 11			
US-09-905-243-6			
Sequence 6, Application US/09905243			
Patent No. 6936698			
GENERAL INFORMATION:			
APPLICANT: Taylor, Alexander H			
TITLE OF INVENTION: Monoclonal Antibodies with Reduced			
TITLE OF INVENTION: Immunogenicity			
FILE REFERENCE: P50770			
CURRENT APPLICATION NUMBER: US/09/905,243			
PRIOR FILING DATE: 2001-07-16			
PRIOR APPLICATION NUMBER: 09/300,970			
PRIOR FILING DATE: 1999-04-28			
NUMBER OF SEQ ID NOS: 97			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 6			
LENGTH: 421			
TYPE: DNA			
ORGANISM: Pan troglodytes			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1)...(421)			
US-09-905-243-6			
Alignment Scores:			
Pred. No.:	1, 116-49	Length:	421
Score:	466.00	Matches:	92
Percent Similarity:	80.8%	Conservative:	13
Best Local Similarity:	70.8%	Mismatches:	13
Query Match:	69.4%	Indels:	12
DB:	3	Gaps:	2
US-10-092-640-32 (1-129) x US-09-905-243-6 (1-421)			
QY	1 GlnValGlnLeuLeuGlnSerGlyValaGluLeuLysProGlyGluSerLeuLysIle	20	
Db	61 GAAGTGCACCTGCTGATGACGTCTGGACCAAGGTAAGAAAGCCCGGGAGTCTTGAAATC	120	
QY	21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet	40	
Db	121 TCTGTGAAGGGTTCGATACAGCTTTCACGATTAAGTGGATGCGCTGGAGTCCCAATG	166	
QY	41 ProGlyLysGlyLeuGlnLysIleMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr	60	
Db	187 CCGGGAAGAGCCTGGAGATGGATGGAGATCATCTGCTGACTCTGATACCAAGATAC	246	
QY	61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr	80	
Db	247 AACCCCTCTTCCCAAGGCCAGGTCAACATCTGACCGCAAGTCCATCAGTACGCGCTAT	306	
QY	81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp	100	
Db	307 TTGCAATGAGAGAGCCTGAAGGCTCGGACACCGCATATGATCTGCGAAGCA---	363	
QY	101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHisTrpGly	120	
Db	364 -----CCGAACGTGGAACTGGTACTTCGTTCTCTGGGGC	396	
QY	121 GlnGlyThrLeuValThr 126		
Db	397 CGTGCACCTGTGCTACT 414		

```

QY 41 ProGlyLyseGlyLeuGlyTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 181 CCGGGGAAAGCCCGGAGTGCATGCGGATCATCTATCTGATGATCTGATACCATAC 240
QY 61 SerProSerPheGlnGlyInValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 241 AGCCCTCTCTCCAAAGGCCAGTCCATCTCAGCCGACAGTCCATCAGCCGCTAC 300
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 301 CTCAATAGAGCAACTGGAAGCCTCGGACACCGCATATATACGTGGAG- 354
QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 118
Db 355 -----TGTATGTTGAGCTACTGCGAAGCTTTGATATC 390
QY 119 TyrGlyGlnGlyThrLeuValThrValSer 128
Db 391 TGGGGCCAAAGGCAATGTCACCGTCTCT 420

RESULT 12
US-08-545-809A-51
; Sequence 51, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasaku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-51

Alignment Scores:
Pred. No.: 5,22e-49 Length: 700
Score: 483.00 Matches: 87

```

```

Percent Similarity: 96.0%
Best Local Similarity: 86.1%
Query Match: 69.0%
DB: 3 Gaps: 0

US-10-092-640-32 (1-129) x US-08-545-809A-51 (1-700)
QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
Db 308 GAGGTCCAGCTGTGTCAGTGTGAGCAGAGGTGAAAAAGCCGGGAGTCTCGAAGATC 367
QY 21 SerCysLyseGlySerGlyTyrSerPheThrSerTyrThrIleAlaTyrValArgIleMet 40
Db 368 TCCGTGAGGGTTCGTGATACAGCTTACCGACTGAGTGGCGCTGGGCGCGAGATG 427
QY 41 ProGlyLyseGlyLeuGlyTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 428 CCGGGGAAAGCCCTGGAAGTGGATGGGATCATCTATCTGATGATCTGATACCATAC 487
QY 61 SerProSerPheGlnGlyInValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 488 AGCCCTCTCTCCAAAGGCCAGTCCATCTCAGCCGACAGTCCATCAGCCGCTAC 547
QY 81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 548 CTGCAGTGAGCAGCTGGAAGCCTCGGACACCGCATATATACGTGGAGACACACA 607
QY 101 Val 101
Db 608 GTG 610

RESULT 13
US-09-515-697-51
; Sequence 51, Application US/09515697
; Patent No. 6936705
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasaku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,697
; FILING DATE: 29-FEB-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid

```


COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-096-762-176

Alignment Scores:

Pred. No.:	2,92e-47	length:	383
Score:	465.50	Matches:	88
Percent Similarity:	85.0%	Conservative:	8
Best Local Similarity:	77.9%	Mismatches:	12
Query Match:	66.5%	Indels:	5
DB:	2	Gaps:	2

US-10-092-640-32 (1-129) x US-08-096-762-176 (1-383)

QY	17	SerLeuLysIleSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrp	36
DB	1	TCTCTGAAGATCTCCGTAAAGGTTCTGATACAGCTTACAGTACGATCGGCTGG	60
QY	37	ValArgGlnMetProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSer	56
DB	61	GTCGCGCAAGATGCCCGGAAAGGCTGAGTGATGGAGATCATCTATCTCGTGACTCT	120
QY	57	AspThrLysTyrSerProSerPheGlnGlyGlnValThrIleSerValAspLysSerVal	76
DB	121	GATACAGATACAGCCCGTCTTCCAAAGCCAGGTACCATCTCAGCCGACAAAGTCCATC	180
QY	77	SerThrAlaTyrLeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCys	96
DB	181	AGACACCGCTACCTGACGAGGAGACAGCTGAAAGGCTCGACACCGCATGTATTAAGTGT	240
QY	97	AlaArgHisAspValGlyTyrCysSerSerSerAsnCysAlaLysTyrProGluTyrPhe	116
DB	241	GGAGAGCGG-----GGGTACTATGTGTGGGGAGTTATTATTAAGTGG-----TTC	285
QY	117	GlnHisTrpGlyGlnGlyThrLeuValThrValSerSer	129
DB	286	GACCCCTGGGCGCAGGAACCTGTCACCGTCTCTCA	324

Search completed: May 25, 2006, 20:50:33
Job time: 169.7 secs

This Page Blank (unused)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 20:50:52 ; Search time 1172.29 Seconds
(without alignments)
2028.220 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700

Sequence: 1 QVQLDSGMELEKKGESLKI.....AKMPYFGHMGCTIVTWS 129

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+;_p2n.model -DEV=xlh
-O=/abs/ABSSWEB.spool/US10092640/runat_25052006_155727_6087/app_query.fasta_1
-DB=Published Applications NA.Main -OPMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TPANS=human4.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pico -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs602h
-USER=US10092640 @CCN 1.1 2326 @runat_25052006_155727_6087 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORE=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YAPOP=10 -YAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	700	100.0	765	3	US-09-888-721-35 Sequence 35, Appl

2	694	99.1	807	3	US-09-888-721-37	Sequence 37, Appl
3	694	99.1	846	3	US-09-888-721-39	Sequence 39, Appl
4	694	99.1	871	3	US-09-888-721-41	Sequence 41, Appl
5	694	99.1	863	3	US-09-888-721-45	Sequence 45, Appl
6	694	99.1	888	3	US-09-888-721-43	Sequence 43, Appl
7	539	77.0	369	13	US-11-009-731-102	Sequence 102, Appl
8	534.5	76.4	660	8	US-10-128-520-298	Sequence 298, Appl
9	532.5	76.1	666	8	US-10-128-520-305	Sequence 305, Appl
10	532.5	76.1	666	8	US-10-128-520-308	Sequence 308, Appl
11	532.5	76.1	672	8	US-10-128-520-308	Sequence 308, Appl
12	531	75.9	669	8	US-10-128-520-286	Sequence 69, Appl
13	530.5	75.8	379	8	US-10-041-860-66	Sequence 33, Appl
14	530.5	75.8	379	8	US-10-665-383-33	Sequence 307, Appl
15	529	75.6	669	8	US-10-128-520-307	Sequence 65, Appl
16	528.5	75.5	379	7	US-10-041-860-65	Sequence 77, Appl
17	528.5	75.5	379	7	US-10-041-860-67	Sequence 25, Appl
18	528.5	75.5	379	8	US-10-665-383-25	Sequence 49, Appl
19	528.5	75.5	379	8	US-10-665-383-49	Sequence 299, Appl
20	528.5	75.5	666	8	US-10-128-520-299	Sequence 298, Appl
21	526.5	75.2	666	8	US-10-128-520-294	Sequence 288, Appl
22	526.5	75.2	672	8	US-10-128-520-288	Sequence 295, Appl
23	526	75.1	369	7	US-10-173-551-3	Sequence 302, Appl
24	526	75.1	669	8	US-10-128-520-295	Sequence 88, Appl
25	525	75.0	669	8	US-10-128-520-302	Sequence 69, Appl
26	523.5	74.8	379	7	US-10-041-860-88	Sequence 311, Appl
27	523.5	74.8	379	8	US-10-665-383-69	Sequence 207, Appl
28	523.5	74.8	666	8	US-10-128-520-311	Sequence 207, Appl
29	520	74.3	462	16	US-11-009-840A-207	Sequence 207, Appl
30	520	74.3	462	16	US-11-009-873A-207	Sequence 207, Appl
31	520	74.3	462	16	US-11-009-873A-207	Sequence 35, Appl
32	519	74.1	351	16	US-11-157-494-37	Sequence 37, Appl
33	519	74.1	351	16	US-11-157-494-37	Sequence 26, Appl
34	519	74.1	469	8	US-10-395-894-26	Sequence 26, Appl
35	519	74.1	469	8	US-10-395-894-26	Sequence 5, Appl
36	519	74.1	469	10	US-10-695-667-26	Sequence 5, Appl
37	519	74.1	7558	8	US-10-395-894-5	Sequence 5, Appl
38	519	74.1	7558	8	US-10-395-894-5	Sequence 5, Appl
39	519	74.1	7558	10	US-10-976-352-5	Sequence 5, Appl
40	518.5	74.1	666	8	US-10-128-520-309	Sequence 309, Appl
41	518	74.0	388	7	US-10-041-860-71	Sequence 71, Appl
42	518	74.0	388	8	US-10-665-383-37	Sequence 37, Appl
43	518	74.0	669	8	US-10-128-520-291	Sequence 291, Appl
44	517	73.9	669	8	US-10-128-520-287	Sequence 287, Appl
45	512.5	73.2	354	7	US-10-181-324-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-888-721-35
; Sequence 35, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Maresco, Wayne A.
; APPLICANT: Scheman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCES: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888, 721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213, 653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Human/murine
OTHER INFORMATION: chimeric single chain binding polypeptide (C6.5
US-09-888-721-35
OTHER INFORMATION: sfv)

Alignment Scores:

Pred. No.:	3,33e-78	Length:	765
Score:	700.00	Matches:	129
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-092-640-32 (1-129) x US-09-888-721-35 (1-765)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGCACAGCTGTGACAGTCTGGGGCAGAGTTGAAAAACCCGGGAGTCTCGAAGATC 60
QY 21 SerCysIlyeGlySerGlyIlyrSerPheThrSerTyrTrrPleAlaTrpValArgGlnMet 40
DB 61 TCCGTGAAGGGTTCTGGAGTACAGCTTTACCACTGATCGCTGGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnIlyrMetGlyLeuIleTyrProGlyYAspSerAspThrIlyrTyr 60
DB 121 CCCGGGAAAGGCTGAGATACATGGGGCTCATCTATCTGTGACTCTGACACCAATATC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 ACCCGGCTCTTCCAAAGGCCAGGTCAACCATCTCAGTCAGCAAGTCCGTGACACTGCTTAC 240
QY 81 LeuGlnIlyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTGCATATGAGCAGATGTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyIlyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGATATGTCAGATGATGTTCCAACTGCCGAAAGTGGCCTGATTACTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGGACCCCTGTGTACCGTCTCTCA 387

RESULT 2

US-09-888-721-37
Sequence 37, Application US/09888721
Patent No. US2002013290A1

GENERAL INFORMATION:

APPLICANT: Huston, James S.

APPLICANT: Zhu, Quan

APPLICANT: Laurent, Olivier

APPLICANT: Marasco, Wayne A.

APPLICANT: Scherman, Daniel

TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID

FILE REFERENCE: 23611-A USA

CURRENT APPLICATION NUMBER: US/09/888,721

PRIOR FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: 60/213,653

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 37

LENGTH: 807

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Human/murine

OTHER INFORMATION: chimeric single chain binding polypeptide (C6ML3-9

OTHER INFORMATION: sfv')

US-09-888-721-37

Alignment Scores:

Pred. No.:	2.06e-77	Length:	807
Score:	694.00 <td>Matches:</td> <td>127</td>	Matches:	127
Percent Similarity:	100.0% <td>Conservative:</td> <td>2</td>	Conservative:	2
Best Local Similarity:	98.4% <td>Mismatches:</td> <td>0</td>	Mismatches:	0
Query Match:	99.1% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	3	Gaps:	0

US-10-092-640-32 (1-129) x US-09-888-721-37 (1-807)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGCACAGCTGTGACAGTCTGGGGCAGAGTTGAAAAACCCGGGAGTCTCGAAGATC 60
QY 21 SerCysIlyeGlySerGlyIlyrSerPheThrSerTyrTrrPleAlaTrpValArgGlnMet 40
DB 61 TCCGTGAAGGGTTCTGGAGTACAGCTTTACCACTGATCGCTGGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnIlyrMetGlyLeuIleTyrProGlyYAspSerAspThrIlyrTyr 60
DB 121 CCCGGGAAAGGCTGAGATACATGGGGCTCATCTATCTGTGACTCTGACACCAATATC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 ACCCGGCTCTTCCAAAGGCCAGGTCAACCATCTCAGTCAGCAAGTCCGTGACACTGCTTAC 240
QY 81 LeuGlnIlyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTGCATATGAGCAGATGTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY 101 ValGlyIlyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB 301 GTGGATATGTCAGATGATGTTCCAACTGCCGAAAGTGGCCTGATTACTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGGACCCCTGTGTACCGTCTCTCA 387

RESULT 3

US-09-888-721-39
Sequence 39, Application US/09888721
Patent No. US2002013290A1

GENERAL INFORMATION:

APPLICANT: Huston, James S.

APPLICANT: Wils, Pierre

APPLICANT: Zhu, Quan

APPLICANT: Laurent, Olivier

APPLICANT: Marasco, Wayne A.

APPLICANT: Scherman, Daniel

TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID

FILE REFERENCE: 23611-A USA

CURRENT APPLICATION NUMBER: US/09/888,721

PRIOR FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: 60/213,653

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 39

LENGTH: 846

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Human/murine

OTHER INFORMATION: chimeric single chain binding polypeptide

OTHER INFORMATION: (C6ML-3-9sfv'-LI-KDEL)

US-09-888-721-39

Alignment Scores:

Pred. No.:	2.19e-77	Length:	846
Score:	694.00 <td>Matches:</td> <td>127</td>	Matches:	127
Percent Similarity:	100.0% <td>Conservative:</td> <td>2</td>	Conservative:	2
Best Local Similarity:	98.4% <td>Mismatches:</td> <td>0</td>	Mismatches:	0

Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-32 (1-129) x US-09-888-721-39 (1-846)

```

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
DB      1 CAGGTGACGTGCTGTCAGTCTGGGGCAGAGTGAAGAAAAAGCCGGGAGTCTTGAAGATC 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValArgGlnMet 40
DB      61 TCCTGTAAGGCTTCTGATACAGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAGCTTAC 120
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuLysTyrProGlyLysSerAspThrLysTyr 60
DB      121 CCGGGAAAGCCCTGGAGTACATGGGGCTCATCTTCCTGTAATCTTGACCAATATAC 180
QY      61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 AGCCGCTCTTCCAAAGCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 240
QY      81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB      241 TTGCAATGAGAGCTGTAAGCCCTCGACAGCCGCTGTAATTTTGTGGAGACATGAC 300
QY      101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB      301 GTGGATATTGAGTGAATTCCTCACTGGCAAGTGGCTGTAATTAATCTTCCAGCATTTGGGC 360
QY      121 GlnGlyThrLeuValThrValSerSer 129
DB      361 CAGGGACCTCTGCTCAGCTCTCTCTCA 387

```

RESULT 4

```

US-09-888-721-41
; Sequence 41, Application US/09888721
; Patent No. US2002013290A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6ML3-9sfv'-L2-KDEL)
US-09-888-721-41

```

Alignment Scores:

```

Pred. No.: 2,24e-77 Length: 861
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0

```

US-10-092-640-32 (1-129) x US-09-888-721-41 (1-861)

```

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
DB      1 CAGGTGACGTGCTGTCAGTCTGGGGCAGAGTGAAGAAAAAGCCGGGAGTCTTGAAGATC 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValArgGlnMet 40
DB      61 TCCTGTAAGGCTTCTGATACAGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAGCTTAC 120
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuLysTyrProGlyLysSerAspThrLysTyr 60
DB      121 CCGGGAAAGCCCTGGAGTACATGGGGCTCATCTTCCTGTAATCTTGACCAATATAC 180
QY      61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB      181 AGCCGCTCTTCCAAAGCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 240
QY      81 LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB      241 TTGCAATGAGAGCTGTAAGCCCTCGACAGCCGCTGTAATTTTGTGGAGACATGAC 300
QY      101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
DB      301 GTGGATATTGAGTGAATTCCTCACTGGCAAGTGGCTGTAATTAATCTTCCAGCATTTGGGC 360
QY      121 GlnGlyThrLeuValThrValSerSer 129
DB      361 CAGGGACCTCTGCTCAGCTCTCTCTCA 387

```

RESULT 5

```

US-09-888-721-45
; Sequence 45, Application US/09888721
; Patent No. US2002013290A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6ML3-9sfv'-L2-nls)
US-09-888-721-45

```

Alignment Scores:

```

Pred. No.: 2,28e-77 Length: 873
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0

```

US-10-092-640-32 (1-129) x US-09-888-721-45 (1-873)

```

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
DB      1 CAGGTGACGTGCTGTCAGTCTGGGGCAGAGTGAAGAAAAAGCCGGGAGTCTTGAAGATC 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTyrValArgGlnMet 40

```

```
Db 61 TCCTGTAAGGCTTCGAGTACAGCTTTACCACTGATGCTGCTGGGTGCGCAGATG 120
Qy 41 ProGlyLysGlyLeuGluIuTyMeGlyLeuIleTyProGlyAspSerAspThrIleTy 60
Db 121 CCGGGGAAAGGCTGGAGTACATGGGGCTCATCTATCTGAGTCTGACACCAATAC 180
Qy 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTy 80
Db 181 AGCCGCTCTTCCAAAGGCCAGGTCAACATCTGACGACAAAGTCCGTGACACTGCTAC 240
Qy 81 LeuGlnIuTySerSerLeuLysProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
Db 241 TTGCATGAGAGCAGTCTGAAGCTTGAAGCCCTGACACGCCGTGATTTTGTGCGAGACATGC 300
Qy 101 ValGlyTyCySerSerSerSerAsnCysAlaTyStrpProGluTyPheGlnHisStrpGly 120
Db 301 GTGGGATATTGAGATGATTCGAATGCCCAAGTGGCTGAATATCTTCAGCATTTGGGGC 360
Qy 121 GlnGlyThrLeuValThrValSerSer 129
Db 361 CAGGGCACCTGTGTCACCGTCTCTCA 387

RESULT 6
US-09-888-721-43
; Sequence 43, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
US-09-888-721-43

Alignment Scores:
Pred. No.: 2,33e-77 Length: 888
Score: 694.00 Matches: 127
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.4% Mismatches: 0
Query Match: 99.1% Indels: 0
Gaps: 0

US-10-092-640-32 (1-129) x US-09-888-721-43 (1-888)
Qy 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
Db 1 CAGGTGACAGCTGTGAGTCTGGGGCAGAGGTGAAAAAGCCCGGAGAGCTCTGAAGATC 60
Qy 21 SerCyLysGlySerGlyTyTrSerPheThrSerTyTrIleAlaTrpValArgGlnMet 40
Db 61 TCTGTGAAGGATTCGATACAGCTTACAGCTACTGGATCGCCGTGGGGCGCCAGATG 120
Qy 41 ProGlyLysGlyLeuGluIuTyMeGlyLeuIleTyProGlyAspSerAspThrIleTy 60
```

```
Db 121 CCGGGGAAAGGCTGGAGTACATGGGGCTCATCTATCCGTGGTACCTGACACCAATAC 180
Qy 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTy 80
Db 181 AGCCGCTCTTCCAAAGGCCAGGTCAACATCTGACGACAAAGTCCGTGACACTGCTAC 240
Qy 81 LeuGlnIuTySerSerLeuLysProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
Db 241 TTGCATGAGAGCAGTCTGAAGCTTGAAGCCCTGACACGCCGTGATTTTGTGCGAGACATGC 300
Qy 101 ValGlyTyCySerSerSerSerAsnCysAlaTyStrpProGluTyPheGlnHisStrpGly 120
Db 301 GTGGGATATTGAGATGATTCGAATGCCCAAGTGGCTGAATATCTTCAGCATTTGGGGC 360
Qy 121 GlnGlyThrLeuValThrValSerSer 129
Db 361 CAGGGCACCTGTGTCACCGTCTCTCA 387

RESULT 7
US-11-009-731-102
; Sequence 102, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shrikant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vandipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MX1-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-009-731-102

Alignment Scores:
Pred. No.: 3,3e-58 Length: 369
Score: 539.00 Matches: 101
Percent Similarity: 89.9% Conservative: 15
Best Local Similarity: 78.3% Mismatches: 7
Query Match: 77.0% Indels: 6
Gaps: 3

US-10-092-640-32 (1-129) x US-11-009-731-102 (1-369)
Qy 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
Db 1 GAGGTGACAGCTGTGAGTCTGGAGCAGAGGTGAAAAAGCCCGGAGAGCTCTGAAGATC 60
Qy 21 SerCyLysGlySerGlyTyTrSerPheThrSerTyTrIleAlaTrpValArgGlnMet 40
Db 61 TCCTGTAAGGCTTCGAGTACAGCTTTCCCACTGATGCTGCTGGGTGCGCAGATG 120
Qy 41 ProGlyLysGlyLeuGluIuTyMeGlyLeuIleTyProGlyAspSerAspThrIleTy 60
Db 121 CCGGGGAAAGGCTGGAGTACATGGGGCTCATCTATCCGTGGTACCTGACACCAATAC 180
Qy 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIleTy 80
Db 181 AGCCGCTCTTCCAAAGGCCAGGTCAACATCTGACGACAAAGTCCGTGACACTGCTAC 240
```

QY	81	LeuGlnTyrSerSerLeuLysProSerAspSerAlaValAlaThrPheCysAlaArgHisAsp	100
Db	241	CTGCAGTGGAGCAGCCTGAAGCGCTCGACACCCGCAATGATTACTGTGGAGA-----	294
QY	101	ValGlyTyrCysSerSerSerAsnCySAAlaLysTyrProGluTyrPheGlnHisTyrGly	120
Db	295	---GGATTATTGTAGAGTGGTGTGAGCTC-----TACCCA---TTCCTCCAGTACTGGGGC	342
QY	121	GInGlyThrLeuValThrValSerSer	129
Db	343	CAGGGCACCTGCTGTCACCTCTCTCTCC	369
RESULT 8			
US-10-128-520-298			
; Sequence 298, Application US/10128520			
; Publication No. US20040105862A1			
; GENERAL INFORMATION:			
; APPLICANT: PAN et al.			
; TITLE OF INVENTION: Human TIMP-1 Antibodies			
; FILE REFERENCE: 02973.00073			
; CURRENT APPLICATION NUMBER: US/10/128,520			
; CURRENT FILING DATE: 2002-04-24			
; PRIOR APPLICATION NUMBER: US 60/285,683			
; PRIOR FILING DATE: 2001-04-24			
; NUMBER OF SEQ ID NOS: 381			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 298			
; LENGTH: 660			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-128-520-298			
Alignment Scores:			
Pred. No.:	2.63e-57	Length:	660
Score:	534.50	Matches:	99
Percent Similarity:	86.0%	Conservative:	12
Best Local Similarity:	76.7%	Mismatches:	7
Query Match:	76.4%	Indels:	11
DB:	8	Gaps:	1
US-10-092-640-32 (1-129) x US-10-128-520-298 (1-660)			
QY	1	GInValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle	20
Db	1	CAGGTGCATATGGTTTCAGAGCGCGCGGAGTGAATAAAACCGGGCGAAACCTGAAAAATT	60
QY	21	SerCyAlaLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTyrValArgGlnMet	40
Db	61	AGCTCAAAAGCTTCGGGATATTCCTTTACGAGTATTGGATTGGCTGGGTGGCCCGCAGATG	120
QY	41	ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr	60
Db	121	CCTGGGAAGGGCTCGAGTGAATGGCATTTATTATCCGGCGCATGCGTATCCGCTTAT	180
QY	61	SerProSerPheGlnGlyGlnAlaThrIleSerValAspLysSerValSerThrAlaTyr	80
Db	181	TCTCCGAGCTTTCAGGGCCAGAGTGACATTAGCGCGGATTAAGCAATTAGCACCGGCTAT	240
QY	81	LeuGlnTyrSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp	100
Db	241	CTTCAATGAGCAGCGCTCGAAACGAGCGCATGATGATATGATGCGGCGCTTAT---	297
QY	101	ValGlyTyrCysSerSerSerAsnCySAAlaLysTyrProGluTyrPheGlnHisTyrGly	120
Db	298	-----CGTATCTCATATGTTGATTTTGTGGGCG	327
QY	121	GInGlyThrLeuValThrValSerSer	129
Db	328	CAGGACACCTGCTGACGGTTAGCTCA	354
RESULT 9			
US-10-128-520-293			
; Sequence 293, Application US/10128520			

```

1 / Publication No. US20040105862A1
2 / GENERAL INFORMATION:
3 / APPLICANT: PAN et al.
4 / TITLE OF INVENTION: Human TIMP-1 Antibodies
5 / FILE REFERENCE: 02973.00073
6 / CURRENT APPLICATION NUMBER: US/10/128,520
7 / CURRENT FILING DATE: 2002-04-24
8 / PRIOR APPLICATION NUMBER: US 60/285,683
9 / PRIOR FILING DATE: 2001-04-24
10 / NUMBER OF SEQ. ID NOS: 381
11 / SOFTWARE: FastSeq for Windows Version 4.0
12 / SEQ ID NO 293
13 / LENGTH: 666
14 / TYPE: DNA
15 / ORGANISM: Homo sapiens
16 / US-10-128-520-293
17
18 Alignment Scores:
19 Pred. No.: 4, 77e-57 Length: 666
20 Score: 532.50 Matches: 100
21 Percent Similarity: 87.6% Conservative: 13
22 Best Local Similarity: 77.5% Mismatches: 7
23 Query Match: 76.1% Indels: 9
24 DB: Gaps: 2
25
26 US-10-092-640-32 (1-129) x US-10-128-520-293 (1-666)
27
28 QY 1 GlnValGlnLeuGlnGlnSerGlyValGlnLeuValysProGlyGlnSerLeuValys 20
29 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
30 Db 1 CAGGTGCATTGGTTATGAGCGCGCCGGAGTGAAGAAAAACCGCGGAAGCTGAAATT 60
31
32 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleaIatrpValArgGlnMet 40
33 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
34 Db 61 AGCTGCAAAAGTTCGCGATATTCCTTTACGAGCTATGATGGTGGTGGCGCCAGATG 120
35
36 QY 41 ProGlyLysGlyLeuGlnLysMetClyLeuLeuIleTyrProGlyAaspSerAspThrLysTyr 60
37 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
38 Db 121 CCGGGAAGAGGTCCTCAGAGTGAAGGGCAATTATTATTCGGGCGAGTAGCGATACCGTTAT 180
39
40 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrIalTyr 80
41 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
42 Db 181 TCTCCAGAGTTTCAGAGGCCAGGTGACATTAGCCGCGAATAAAGCATTTAGCAGCCGCTAT 240
43
44 QY 81 LeuGlnTTPSerSerLeuLysProSerAaspSerAlaValTyrPheCysAlaArgHisAsp 100
45 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
46 Db 241 CTTCAATGAGCAGACCTGAACCGAGCATACGCGCAATGATTTATGTGGCGCGCTTAT--- 297
47
48 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTyrProGlyLysPheGlnHisTyrGly 120
49 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
50 Db 298 -----TATGTTACTGATACT-----GCTTATTTGATTATTTGGGGC 333
51
52 QY 121 GlnGlyThrLeuValThrValSerSer 129
53 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
54 Db 334 CAAGGCACCCGTGTGACGGTTAGCTCA 360
55
56 RESULT 10
57 US-10-128-520-305
58 / Sequence 305, Application US/10128520
59 / Publication No. US20040105862A1
60 / GENERAL INFORMATION:
61 / APPLICANT: PAN et al.
62 / TITLE OF INVENTION: Human TIMP-1 Antibodies
63 / FILE REFERENCE: 02973.00073
64 / CURRENT APPLICATION NUMBER: US/10/128,520
65 / CURRENT FILING DATE: 2002-04-24
66 / PRIOR APPLICATION NUMBER: US 60/285,683
67 / PRIOR FILING DATE: 2001-04-24
68 / NUMBER OF SEQ. ID NOS: 381
69 / SOFTWARE: FastSeq for Windows Version 4.0
70 / SEQ ID NO 305
71 / LENGTH: 666
72 / TYPE: DNA
73 / ORGANISM: Homo sapiens

```

US-10-128-520-305

Alignment Scores:
Pred. No.: 4.77e-57 Length: 666
Score: 532.50 Matches: 101
Percent Similarity: 84.8% Conservative: 11
Best Local Similarity: 76.5% Mismatches: 5
Query Match: 76.1% Indels: 15
DB: 8 Gaps: 2

US-10-092-640-32 (1-129) x US-10-128-520-305 (1-666)

```
OY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
Db 1 CAGGTGCATTGGTTTCAGAGCGCGCGGAGTCAAAAAACCGGCGAAAGCTGAAAAATT 60
OY 21 SerCyLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 ACCTGCAAGGTTCCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 120
OY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuLysTyrProGlyLysSerAspThrLysTyr 60
Db 121 CCGGAAAGGCTCTCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 180
OY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 TCTCCGAGCTTTCAGGCGCAGGTGACCATTTAGCGCGGATTAAGCATTTAGCACCGGCTAT 240
OY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 CTTCAATGAGCAGCCTGAAAGCGAGCATACGCGCATGATATTTAGCGCGCT----- 294
OY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 117
Db 295 -----CTTTATCCGAGATCTTATTTATTTTGAT 324
OY 118 HisTrpGlyGlnGlyThrLeuValThrValSerSer 129
Db 325 TATTTGGGCGCAAGCGACCTGTGTGACGGTTAGCTCA 360
```

RESULT 11

US-10-128-520-308
; Sequence 308, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-520-308

Alignment Scores:

Pred. No.: 4.82e-57 Length: 672
Score: 532.50 Matches: 102
Percent Similarity: 86.8% Conservative: 10
Best Local Similarity: 79.1% Mismatches: 10
Query Match: 76.1% Indels: 7
DB: 8 Gaps: 2

US-10-092-640-32 (1-129) x US-10-128-520-308 (1-672)

```
OY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
Db 1 CAGGTGCATTGGTTTCAGAGCGCGCGGAGTCAAAAAACCGGCGAAAGCTGAAAAATT 60
```

```
OY 21 SerCyLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 ACCTGCAAGGTTCCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 120
OY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuLysTyrProGlyLysSerAspThrLysTyr 60
Db 121 CCGGAAAGGCTCTCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 180
OY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 TCTCCGAGCTTTCAGGCGCAGGTGACCATTTAGCGCGGATTAAGCATTTAGCACCGGCTAT 240
OY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 CTTCAATGAGCAGCCTGAAAGCGAGCATACGCGCATGATATTTAGCGCGCTTTT--- 297
OY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db 298 GTTCTTATTAATGTTCT-----GTTCTTATTTGATTTAGTGGGCG 339
OY 121 GlnGlyThrLeuValThrValSerSer 129
Db 340 CAAGGCACCTGTGTGACGGTTAGCTCA 366
```

RESULT 12

US-10-128-520-286
; Sequence 286, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-520-286

Alignment Scores:

Pred. No.: 7.43e-57 Length: 669
Score: 531.00 Matches: 101
Percent Similarity: 86.0% Conservative: 10
Best Local Similarity: 78.3% Mismatches: 10
Query Match: 75.9% Indels: 8
DB: 8 Gaps: 2

US-10-092-640-32 (1-129) x US-10-128-520-286 (1-669)

```
OY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
Db 1 CAGGTGCATTGGTTTCAGAGCGCGCGGAGTCAAAAAACCGGCGAAAGCTGAAAAATT 60
OY 21 SerCyLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 ACCTGCAAGGTTCCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 120
OY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuLysTyrProGlyLysSerAspThrLysTyr 60
Db 121 CCGGAAAGGCTCTCGAGTATTCCTTACGAGCTATTGGATTGGCTGGGTCGCCAGATG 180
OY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 TCTCCGAGCTTTCAGGCGCAGGTGACCATTTAGCGCGGATTAAGCATTTAGCACCGGCTAT 240
OY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
```

[illegible]

```

RESULT 14
US-10-665-383-33
; Sequence 33, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Fioege, Uerger
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: AGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 379
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-665-383-33

Alignment Scores:
Pred. No.: 4,08e-57 Length: 379
Score: 530.50 Matches: 99
Percent Similarity: 86.0% Conservative: 12
Best Local Similarity: 76.7% Mismatches: 15
Query Match: 75.8% Indels: 3
Gaps: 8

US-10-092-640-32 (1-129) x US-10-665-383-33 (1-379)
QY 1 GlnValGlnLeuLeuGlnSerGlyValGlnLeuLysLysProGlyGlnSerLeuLysIle 20
Db 1 GAGGTCCAGCTGGTGCAGTCCGGGACACAGTGAAGAAAGCCCGGAGACTCTCTAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
Db 61 TCCCTGAAGGGTTCGAGATACAGGTTTACCAAGTCTGAGTCCGCTGGTCCGCAATG 120
QY 41 ProGlyLysGlyLeuGlnTyrMetCysLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db 121 CCGGGAAAGGCGCTGGAGGATGGGGATCATCTATCTGTGGACTGTGATACCAAGTAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db 181 AGCCCTCTCTTCMAAGGCCAGGTACCATCTCAGCCGACAAAGTCCATCAGCACCGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db 241 CTCGATGGAGAGACGCTGAAAGGCGCTCGACACCGCCAGTATTACTGTGCGAGACATGA 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyTyrPheGlnHisTrpGly 120
Db 301 TCGTATTATTATGATGTTCCGAGACT-----TATTATAATGCTTTGACTACTGGGCG 351
QY 121 GlnGlyThrLeuValThrValSerSer 129
Db 352 CAGGGAACTCTGTCACTCCCTCTCA 378

RESULT 15
US-10-128-520-307
; Sequence 307, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520

```

```

? CURRENT FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: US 60/285,683
? PRIOR FILING DATE: 2001-04-24
? NUMBER OF SEQ ID NOS: 381
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 307
? LENGTH: 669
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-128-520-307

```

Alignment Scores:	
Pred. No.:	1.33e-56
Score:	529.00
Percent Similarity:	84.1%
Best Local Similarity:	76.5%
Query Match:	75.6%
DB:	8
Gaps:	2
Length:	666
Matches:	101
Conservative:	10
Mismatches:	7
Indels:	14
Gaps:	2

US-10-092-640-32 (1-129) X US-10-128-520-307 (1-669)

QY		1	GlnValGlnLeuLeuGlnSerLysIleAspLeuValySlyProGlyHisSerLeuIle	20
Db		1	CAGGGCAATTGGTTCAGACCGGCCGGAGAAGTAATAAACCCGGCCGAACCTCGAATTT	60
QY		21	SerCysLySGlySerGIYTrSerPheThrSerTYrTpIleAlaIrrValAArgImet	40
Db		61	AGCTCAAGAAGGTCCGGAATATTCCTTTACAGACTATTGATGGCTGGGGCCGCAGATG	120
QY		41	ProGlyLyvSGlyLeuGluTyrmMetGlyLeuIleTYrProGlyAspSerAspThrySTyr	60
Db		121	CCTGGAAAGGCGTCGAGTGATGGCATTTATTTACCGGGCCATGACGATACCCTTAT	180
QY		61	SerProSerPheGlnGlyGlnValThrIleSerValAspSlySerValSerThrAlaTYr	80
Db		181	TCTCCGAGCTTTCAGAGCCAGGTGACCATTTAGCGCGAATAAAGCATTTGACACCGGGTAT	240
QY		81	LeuGlnTrpSerSerLeuylsPseroSerAspSerAlaValTYrPhcYSalaArg-----	98
Db		241	CTTCATATGAGCAGGCTGAAAACGACGATACGGCCATGATATTTGGCGGCGTCTTCGT	300
QY		99	--HisaspValGlyTYrCysserSerSerashnCysAlalySrTrpProGluTyrrpheGln	117
Db		301	GTTTCATGTAT-----TATGCTATGATTTTGTAT	327
QY		118	HistRpglyGlnGlyThrleuValThrValSerSer	129
Db		328	CTTGGGGGCCAAGGACCCCTGGTGAAGGTTTAGCTCA	363

Search completed: May 25, 2006, 21:27:51
Job time : 1174.29 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_pzn model

Run on: May 25, 2006, 20:51:32 ; Search time 20.425 Seconds
(without alignments)
1069.431 Million cell updates/sec

Title: US-10-092-640-32
Perfect score: 700
Sequence: 1 QVQLQSGAELKKRGESLKI.....AKMPEYFQHWGQGLTVVSS 129

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ pzn.model -DEV=xlh
-Q=/abs/ABSSWEB.spool/US10092640/runat_25052006_155730_6141/app_query.fasta_1
-DB=Published Applications NA New -OPMT=fastcap -SUFFIX=rnphn -MINMATCH=0.1
-LOOPT=0 -LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs802h
-USER=US10092640 @CGN 1.1.26 @runat_25052006_155730_6141 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=10
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
1: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US09_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/Pctodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	69.6	369	6	US-10-499-266-11 Sequence 11, Appl
2	406.5	58.1	378	7	US-11-211-917-41 Sequence 41, Appl
3	406.5	58.1	1416	7	US-11-211-917-45 Sequence 45, Appl
4	398.5	56.9	2094	7	US-11-155-444-1 Sequence 1, Appl1
5	398.5	56.9	2196	7	US-11-155-444-5 Sequence 5, Appl1
6	390.5	55.8	885	7	US-11-154-103-33 Sequence 33, Appl
7	374	53.4	420	7	US-11-183-218-61 Sequence 61, Appl
8	374	53.4	9209	7	US-11-183-218-58 Sequence 58, Appl
9	368.5	52.6	726	7	US-11-183-325-17 Sequence 17, Appl

10	368.5	52.6	756	7	US-11-330-353-17	Sequence 17, Appl
11	365.5	52.2	372	7	US-11-271-008-10	Sequence 10, Appl
12	364.5	52.1	333	7	US-11-216-003-13	Sequence 13, Appl
13	361.5	51.6	360	7	US-11-221-902-83	Sequence 83, Appl
14	358.5	51.2	354	7	US-11-297-317-12	Sequence 12, Appl
15	358.5	51.2	8687	7	US-11-297-317-15	Sequence 15, Appl
16	356.5	50.9	360	7	US-11-221-902-20	Sequence 20, Appl
17	355.5	50.8	354	7	US-11-297-317-11	Sequence 11, Appl
18	355.5	50.8	8687	7	US-11-297-317-16	Sequence 16, Appl
19	352	50.3	807	7	US-11-219-563-23	Sequence 23, Appl
20	352	50.3	807	7	US-11-219-563-24	Sequence 24, Appl
21	352	50.3	1578	7	US-11-219-563-131	Sequence 131, Appl
22	352	50.3	1701	7	US-11-106-662-10	Sequence 10, Appl
23	349.5	49.9	360	7	US-11-221-902-82	Sequence 82, Appl
24	341.5	48.8	333	7	US-11-216-003-9	Sequence 9, Appl1
25	338.5	48.4	354	7	US-11-297-317-6	Sequence 6, Appl1
26	338.5	48.4	1362	6	US-10-981-300-15	Sequence 15, Appl
27	335.5	47.9	726	7	US-11-183-325-19	Sequence 19, Appl
28	335	47.9	408	7	US-11-315-067-1	Sequence 1, Appl1
29	335	47.9	408	7	US-11-315-067-7	Sequence 7, Appl1
30	333	47.6	873	7	US-11-154-103-35	Sequence 35, Appl
31	331.5	47.4	1628	7	US-11-293-697-1846	Sequence 1846, Ap
32	331	47.3	1602	7	US-11-293-697-1849	Sequence 1849, Ap
33	330.5	47.2	360	7	US-11-254-679-16	Sequence 16, Appl
34	329	47.0	1613	7	US-11-293-697-1839	Sequence 1839, Ap
35	326	46.6	873	7	US-11-154-103-36	Sequence 36, Appl
36	326	46.6	1618	7	US-11-293-697-1845	Sequence 1845, Ap
37	325	46.4	1613	7	US-11-293-697-1848	Sequence 1848, Ap
38	323.5	46.2	366	7	US-11-254-679-73	Sequence 73, Appl
39	322.5	46.1	378	7	US-11-254-679-49	Sequence 49, Appl
40	322	46.0	1598	7	US-11-293-697-1642	Sequence 1642, Ap
41	321	45.9	360	7	US-11-254-679-12	Sequence 12, Appl
42	319.5	45.6	369	7	US-11-254-679-69	Sequence 69, Appl
43	319.5	45.6	873	7	US-11-154-103-32	Sequence 32, Appl
44	318.5	45.5	354	7	US-11-219-563-73	Sequence 73, Appl
45	318.5	45.5	354	7	US-11-219-563-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-10-499-266-11
; Sequence 11, Application US/10499266
; Publication No. US20060088531A1
; GENERAL INFORMATION:
; APPLICANT: Smethurst, Peter Alexander
; APPLICANT: Ouweland, Willem Hendrik
; APPLICANT: Parndale, Richard William
; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST HUMAN
; FILE REFERENCE: 19134.401USPC
; CURRENT APPLICATION NUMBER: US/10/499,266
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/GB02/05755
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: GB 0130543.2
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-499-266-11

Alignment Scores:
Pred. No.: 1,1e+48
Score: 487.00
Percent Similarity: 78.9%
Best Local Similarity: 70.7%
Query Match: 69.6%
DB: 6
Length: 369
Matches: 94
Conservative: 11
Mismatch: 14
Indels: 14
Gaps: 2

```

US-10-092-640-32 (1-129) x US-10-499-266-11 (1-369)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
      1 CAGGTACAGACTGAGAGCTCAGGGGCGAGGTGAAGAAAGCCGGGGAGCTCTGAAGATC 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      61 TCTGTACAGGCTTCTGATACAGCTTTCAGATTCTGATGCGCTGGGTGGCGCAGATG 120
QY      41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
      121 CCGGGAAAGGCGCTGGAGTTGATGGGATCATCTATCTGATGACCTGATGCGAGATAC 180
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      181 ACCCGGCTCTTCCAGGCGCAGGTGACCTTCTCAGCCGACAGCCATMAACACCGGCTAT 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
      241 TTGCAAGTGAAGACGCTTGAGAGGCTTGAGACCGCATGATATTGTGCGAGACAA--- 297
QY      101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLysTyr-----Phe 116
      298 -----GGGAAAACTGGAGGCTACTATTGTTGGTCTTTT 330
QY      117 GlnHisTrpGlyGlnGlyThrLeuValThrValSerSer 129
      331 GATGCTGGGGCCAGGAGCAATGTCACCGCTCTTCA 369
Db
RESULT 2
US-11-211-917-41
; Sequence 41, Application US/11211917
; Publication No. US2006093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-41

Alignment Scores:
Pred. No.:      2,82e-39      Length:      378
Score:          406.50      Matches:      75
Percent Similarity: 76.9%      Conservative: 25
Best Local Similarity: 57.7%      Mismatches: 25
Query Match:    58.1%      Indels:      5
                        Gaps:      2

US-10-092-640-32 (1-129) x US-11-211-917-41 (1-378)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
      1 CAGGTACAGCTGCTGAGTCTGGGGCTGAGGTGAAGAAGCTTGGGGCTCTCAGTGAAGTTC 60
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      61 TCTGTCAAGGCTTCTGATACACCTTACCGGCTACTATATGACACTGGGTGGCAGACAGGCC 120

```

```

QY      41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
      121 CTTGACAAAGGCTTGAATGATGGATGAGTGAACCTTGACAGTGGTGGCACAACCTAT 180
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      181 GCACAGAAAGTTTCAGGGCAGGGTCAACCATGACACAGGACACGTCATCAGCACACCTAC 240
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArg--His 99
      241 ATGAGCTGAACAGGCTGAGATCTGACGACACGGCGGTGATTACTGTGCGAGATACG 300
QY      100 AspValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlyLysTyrPheGlnHisTrp 119
      301 CCGCTGAGATATTGTACTAAATGTGTATGCTCC-----TACTTGTACTACTGG 348
QY      120 GlyGlnGlyThrLeuValThrValSerSer 129
      349 GGCCAGGAGACCTTGTCACCGTCTCTCA 378
Db
RESULT 3
US-11-211-917-45
; Sequence 45, Application US/11211917
; Publication No. US2006093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-45

Alignment Scores:
Pred. No.:      1.72e-38      Length:      1416
Score:          406.50      Matches:      75
Percent Similarity: 76.9%      Conservative: 25
Best Local Similarity: 57.7%      Mismatches: 25
Query Match:    58.1%      Indels:      5
                        Gaps:      2

US-10-092-640-32 (1-129) x US-11-211-917-45 (1-1416)
QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 20
      58 CAGGTACAGCTGCTGAGTCTGGGGCTGAGGTGAAGAAGCTTGGGGCTCTCAGTGAAGTTC 117
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
      118 TCTGTCAAGGCTTCTGATACACCTTACCGGCTACTATATGACACTGGGTGGCAGACGCC 177
QY      41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
      178 CTTGACAAAGGCTTGAATGATGGATGATGATCAACCTTGACAGTGGTGGCACAACCTAT 237
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
      238 GCACAGAAAGTTTCAAGGCGAGGCTCACATGACAGGAGACAGTCCATGACAGCACGCTAC 297

```



```

Oy      81 LeuGlnTTPSerSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaIaG---Hle 99
Db      298 ATGAGCTCAACACAGCTGAGTGAATCTGCACGACCGCGTGATTAATCTGTGGAGAGATCAG 357
Oy      100 AspValGlyTyrCysSerSerSerAenCysAlaLysTTPProGluTyrPheGlnHisTTP 119
Db      358 CCCCTAGGATTAATGTACTAATGATGGTATGCTCC-----TACTTTGACTACTGG 405
Oy      120 GlyGlnGlyThrLeuValThrValSerSer 129
Db      406 GCCCAGGGAACCTGTGTCACCGTCTCTCA 435

RESULT 4
US-11-155-444-1
; Sequence 1, Application US/11155444
; Publication No. US20060104971A1
; GENERAL INFORMATION:
;   APPLICANT: GABER, ELLEN
;   APPLICANT: BAILLY, VERONIQUE
;   APPLICANT: BROWNING, JEFFREY L.
;   TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
;   FILE REFERENCE: BGNAL68CN
;   CURRENT APPLICATION NUMBER: US/11/155,444
;   PRIOR FILING DATE: 2005-06-17
;   PRIOR APPLICATION NUMBER: PCT/US03/041393
;   PRIOR FILING DATE: 2003-12-22
;   PRIOR APPLICATION NUMBER: 60/435,154
;   PRIOR FILING DATE: 2002-12-20
;   PRIOR APPLICATION NUMBER: 60/435,185
;   PRIOR FILING DATE: 2002-12-20
;   NUMBER OF SEQ ID NOS: 23
;   SOFTWARE: PatentIn Ver. 3.3
;   SEQ ID NO 1
;   LENGTH: 2094
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
US-11-155-444-1

Alignment Scores:
Pred. No.:      2,52e-37      Length:      2094
Score:          398.50      Matches:      75
Percent Similarity: 75.2%      Conservative: 22
Best Local Similarity: 58.1%      Mismatches: 19
Query Match:    56.9%      Indels:      13
Db:             7          Gaps:      2

US-10-092-640-32 (1-129) x US-11-155-444-1 (1-2094)
Oy      1 GlnValGlnLeuLeuGlnSerGlyLysGlnLeuLysProGlyGlnSerLeuLysIle 20
Db      1378 CAGGTCCTCACTGCTGCTGCTGAGCTGAGGTGAGAGAACCTCGGTCCTCAGTGAAGGTG 143
Oy      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTTPIleAlaTTPValArgGlnMet 40
Db      1438 TCCTGCAAGGCTTCTGGCTACACTTTCACAACTACTATTTGGACTGGGAGGCGAGGCC 149
Oy      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysSerAspThrIleTyr 60
Db      1498 CCTGGACGGGACTTGAAGTGAATGGATGATTATCTCGGAATGTTGATGCTCAGTAC 155
Oy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db      1558 AATGGAAGTTCAAGGCGCAGGCTCACATCTACGTCGACGAACAATCCACCGACAGGCTAC 161
Oy      81 LeuGlnTTPSerSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaIaRghHisAsp 100
Db      1618 ATGAGCTCAGCAGCTGAGCTGAGTGAAGTACTGGCGGTCTATTAATCACTGTCACAGA----- 167
Oy      101 ValGlyTyrCysSerSerSerSerAenCysAlaLysTTPProGluTyrPheGlnHisTTPGly 120

```

DB	Accession	Gene	Protein	Length	Matches	Conservative	Mismatches	Gaps
Db	1672	-----TCCTGG--	GAAGGTTTCTTACTGGGCG	1698				
QY	121	GlnGlyThrLeuValThrValSerSer	129					
Db	1699	CAAGGACCAACGCTGCACGCTTCTCTCA	1725					
RESULT 5	US-11-155-444-5							
	/ Sequence 5, Application US/11155444							
	/ Publication No. US20060104971A1							
	/ GENERAL INFORMATION:							
	APPLICANT: GABER, ELLEN							
	APPLICANT: BALLY, VERONIQUE							
	APPLICANT: BROWNING, JEROMEY L.							
	TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND							
	TITLE OF INVENTION: THERAPEUTIC USES THEREOF							
	FILE REFERENCE: BGMA168CN							
	CURRENT APPLICATION NUMBER: US/11/155,444							
	CURRENT FILING DATE: 2005-06-17							
	PRIOR APPLICATION NUMBER: PCT/US03/041393							
	PRIOR FILING DATE: 2003-12-22							
	PRIOR APPLICATION NUMBER: 60/435,154							
	PRIOR FILING DATE: 2002-12-20							
	PRIOR APPLICATION NUMBER: 60/435,185							
	NUMBER OF SEQ ID NOS: 23							
	SOFTWARE: PatentIn Ver. 3.3							
	SEQ ID NO 5							
	LENGTH: 2196							
	TYPE: DNA							
	ORGANISM: Artificial Sequence							
	FEATURE:							
	/ OTHER INFORMATION: Description of Artificial Sequence: huCB2B1/huBHA10							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							
	US-11-155-444-5							
	/							
	/ OTHER INFORMATION: bispecific-2 antibody construct							

```

Db      1801 CAAGGAGCAGCGTCACTCTCTCA 1827

RESULT 6
US-11-154-103-33
; Sequence 33, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-33

Alignment Scores:
Pred. No.: 6,66e-37 Length: 885
Score: 390.50 Matches: 77
Percent Similarity: 75.6% Conservative: 22
Best Local Similarity: 58.8% Mismatches: 25
Query Match: 55.8% Indels: 7
DB: Gaps: 2

US-10-092-640-32 (1-129) x US-11-154-103-33 (1-885)

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      67 GAGGTGCACCTGCTGTCAGTCTGGGGCTGAGTGAAAGCCTGGTCTCTGGAAGGTC 126
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
       |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      127 TCCTGCAAGGCTTCTGAGGACACCTTCAGCAGCTATCTATCAGCTGGGTCGACAGGCC 186
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      187 CCTGGACAGAGCCTTGAGTGGATGGAGGAGATCATCTCTTTGGTACAGCAACTAC 246
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      247 GCACAGAAAGTCCAGGCGCAGAGTCAAGATTACCGCGAGCAAAATCCACGAGCACGCTAC 306
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      307 ATGAGAGTGAAGCCTGAGATCTGAGACACGCGCTGTATTAATCTGTCGAGAGAGGAG 366
QY      101 ValGlyTyrCysSerSerSerSerAsnCySA1AlaLysTrpProGluTyr-----PheGlnHis 118
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      367 GGGGCCATATTGATGATGACCACTGC-----TATGGGGCTTTTGATATC 411
QY      119 TrpGlyGlnGlyThrLeuValThrValSerSer 129
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      412 TGGGGCCAAGGCACTCTGTGTACCCGTCTCTCA 444

RESULT 7
US-11-183-218-61
; Sequence 61, Application US/11183218
; Publication No. US2006008906A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-183-218-61

Alignment Scores:
Pred. No.: 2.03e-35 Length: 420
Score: 374.00 Matches: 74
Percent Similarity: 71.3% Conservative: 18
Best Local Similarity: 57.4% Mismatches: 29
Query Match: 53.4% Indels: 8
DB: Gaps: 2

US-10-092-640-32 (1-129) x US-11-183-218-61 (1-420)

QY      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      58 CAGGTAAACCTGACACAGCTGGGGCTGAGTGGAGCCCTGGGCTCACTGGAAGATG 117
QY      21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      118 TCCTGCAAGGCTTCTGAGTACATTTACCACTTACATATGACACTGGGTAAACAGACA 177
QY      41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      178 CCTGTGCGGGCTCGAATGATGTGAGCTATTATCCGGAATGATGATCTTCTAC 237
QY      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      238 AATCAGAAATTCAGAGGACACATTGACGACAAATCTCCAGACACAGCTAC 297
QY      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      298 ATGACGCTCAGACGCTGACATCTGAGACTCTGGGCTTATCTATCTGCAAGA----- 351
QY      101 ValGlyTyrCysSerSerSerSerAsnCySA1AlaLysTrpProGluTyrPheGlnHisTrpGly 120
       |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

Db 352 -----TCGACTTACTACGGCGGTGACTG-----TACTTCATGCTGTGGGC 393

Qy 121 GlnGlyThrLeuValThrValSerSer 129

Db 394 GCAGGAGCCACGCTCACCGTCTCTGCA 420

RESULT 8

US-11-183-218-58

/ Sequence 58, Application US/11183218

/ Publication No. US20060088906A1

/ GENERAL INFORMATION:

/ APPLICANT: Neose Technologies, Inc.

/ APPLICANT: Defrees, Shawn

/ APPLICANT: Zopf, David

/ APPLICANT: Bayer, Robert

/ APPLICANT: Hakes, David

/ APPLICANT: Chen, Xi

/ APPLICANT: Bove, Caryne

/ TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND

/ TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN

/ FILE REFERENCE: 040853-01-5083-US02

/ CURRENT APPLICATION NUMBER: US/11/183,218

/ PRIOR FILING DATE: 2005-07-15

/ PRIOR APPLICATION NUMBER: US 10/410,945

/ PRIOR FILING DATE: 2003-04-09

/ PRIOR APPLICATION NUMBER: PCT/US02/32263

/ PRIOR FILING DATE: 2002-10-09

/ PRIOR APPLICATION NUMBER: US 60/407,527

/ PRIOR FILING DATE: 2002-08-28

/ PRIOR APPLICATION NUMBER: US 60/404,249

/ PRIOR FILING DATE: 2002-08-16

/ PRIOR APPLICATION NUMBER: US 60/396,594

/ PRIOR FILING DATE: 2002-07-17

/ PRIOR APPLICATION NUMBER: US 60/391,777

/ PRIOR FILING DATE: 2002-06-25

/ PRIOR APPLICATION NUMBER: US 60/387,292

/ PRIOR FILING DATE: 2002-06-07

/ PRIOR APPLICATION NUMBER: US 60/344,692

/ PRIOR FILING DATE: 2001-11-19

/ PRIOR APPLICATION NUMBER: US 60/334,301

/ PRIOR FILING DATE: 2001-11-28

/ PRIOR APPLICATION NUMBER: US 60/334,233

/ PRIOR FILING DATE: 2001-11-28

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 75

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 58

/ LENGTH: 9209

/ TYPE: DNA

/ ORGANISM: Mus musculus

US-11-183-218-58

Alignment Scores:

Pred. No.: 1,38e-33 Length: 9209

Score: 374.00 Matches: 74

Percent Similarity: 71.3% Conservative: 18

Best Local Similarity: 57.4% Mismatches: 29

Query Match: 53.4% Indels: 8

DB: 7 Gaps: 2

US-10-092-640-32 (1-129) x US-11-183-218-58 (1-9209)

Qy 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20

Db 2458 CAGGTCAACAGCTGACAGCGCTGAGCTGTAAGCTGGGCTCAGTGAAGANG 2517

Qy 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40

Db 2518 TCTGTGAAGGCTTCTGGCTACACATTTCAGATTACAAATATGCACTGGGGTAAACAGACA 2577

Qy 41 ProGlyLysGlyLeuGlnLysTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60

Db 2578 CCGTGGCGGGGCTGGAATGATGTAGAGCATTTATCCGGAATGTGTACTTCTCTAC 2637

Qy 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80

Db 2638 AATCAAGATTCAAAAGCAAGCCACATTGATGACGACAAATCCCTCCACACAGCTTAC 2697

Qy 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100

Db 2698 ATGCAGCTCGACGCGCTGACATCTGAGACTCTGCGGTCTATTACTGTGCAAGA----- 2751

Qy 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120

Db 2752 -----TCGACTTACTACGGCGGTGACTG-----TACTTCATGCTGTGGGC 2793

Qy 121 GlnGlyThrLeuValThrValSerSer 129

Db 2794 GCAGGAGCCACGCTCACCGTCTCTGCA 2820

RESULT 9

US-11-183-325-17

/ Sequence 17, Application US/11183325

/ Publication No. US20060104898A1

/ GENERAL INFORMATION:

/ APPLICANT: Vanderbilt University

/ APPLICANT: Hallahan, Dennis E

/ APPLICANT: Qi, Shimian

/ TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES

/ FILE REFERENCE: 1242/47/2/2 CIP

/ CURRENT APPLICATION NUMBER: US/11/183,325

/ PRIOR FILING DATE: 2005-07-15

/ PRIOR APPLICATION NUMBER: US 60/328123

/ PRIOR FILING DATE: 2001-10-03

/ PRIOR APPLICATION NUMBER: US 10/259,087

/ PRIOR FILING DATE: 2002-09-27

/ NUMBER OF SEQ ID NOS: 56

/ SOFTWARE: PatentIn version 3.3

/ SEQ ID NO 17

/ LENGTH: 726

/ TYPE: DNA

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Artificial antibody ligand number 1

/ NAME/KEY: CDS

/ LOCATION: (1)..(726)

US-11-183-325-17

Alignment Scores:

Pred. No.: 1,88e-34 Length: 726

Score: 368.50 Matches: 73

Percent Similarity: 71.3% Conservative: 19

Best Local Similarity: 56.6% Mismatches: 26

Query Match: 52.6% Indels: 11

DB: 7 Gaps: 2

US-10-092-640-32 (1-129) x US-11-183-325-17 (1-726)

Qy 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20

Db 7 CAGGTCAACAGCTGACAGCGCTGAGCTTGTGATGCTCGGGCTCAGTGAAGANG 66

Qy 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40

Db 67 TCTGTGAAGGCTTCTGGCTACACATTTCAGATTACAAATATGCACTGGGGTAAACAGAG 126

Qy 41 ProGlyLysGlyLeuGlnLysTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60

Db 127 CCGTGAAGGCTTCTGGCTACAGGATTCGAGGATGATCTCTCGATATGATCTAGCTTAC 186

Qy 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80

Db 187 AATCAAAAGTTCAAGGCAAGCCACATTGATGTAGAGATCCCTCCAGCACAGCTTAC 246

Qy 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100


```

Db      1 CAGGCCAGCTGCTGCAAGTCTGGGGCTGAAGTGAAGAGCTGGGGCTCAAGTGAAGCTC 60
Qy      21 SerCyAlsyGlySerGlyTyrSerPheThrSerTyrTriPleAlaTrpValArgGlnMet 40
Db      61 TCCTGAAGGCTTCTGGATACACCTTCATCGGCTATTGATGACCTGGGTGGCAGAGGCC 120
Qy      41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db      121 CCGGACAAAGGGCTGAGTGAATGGACGAGTCAACCCCTAACAGTGTGGCACAAGTAT 180
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db      181 GTACAGAACTTCAAGGCGACGGCTACCGTACCAAGGACACGTCCTCACCACAGCCTTAC 240
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
Db      241 ATGAGACTGCAACTGGCTGACATCTGACGACACGGCCGCTATTACTGTGGAGAGCAAG 300
Qy      101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db      301 CTTGGT-----TGCGTGTGTGATTGCTAT-----GAGGTCTTAGATTACTGGGCC 345
Qy      121 GlnGlyThrLeuValThrValSerSer 129
Db      346 CAGGGAACCTGTGCTCACCGTCTCTCA 372

```

RESULT 12

```

US-11-216-033-13
; Sequence 13, Application US/11216033
; Publication No. US20060104899A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GRIFFITHS, GARY L.
; APPLICANT: MCBRIDE, WILLIAM J.
; APPLICANT: LEUNG, SHUI-ON
; APPLICANT: OU, ZHENGXING
; TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
; FILE REFERENCE: 40923-0074US4
; CURRENT APPLICATION NUMBER: US/11/216,033
; PRIOR FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US/09/823,746
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/337,756
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 13
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(333)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized
; OTHER INFORMATION: Mu-9 heavy chain variable region nucleotide sequence
US-11-216-033-13

```

Alignment Scores:

```

Pred. No.: 1 89e-34 Length: 333
Score: 364.50 Matches: 69
Percent Similarity: 68.8% Conservative: 19
Best Local Similarity: 53.9% Mismatches: 23
Query Match: 52.1% Indels: 17
DB: 7 Gaps: 1

```

US-10-092-640-32 (1-129) x US-11-216-033-13 (1-333)

```

Qy      2 ValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIleSer 21
Db      1 GTGCAAGCTCAGACAGTCAAGAGCTGAGTGAAGAAAGCCCTGGAGCTCACTGAAGAGTCTCC 60

```

```

Qy      22 CyAlsyGlySerGlyTyrSerPheThrSerTyrTriPleAlaTrpValArgGlnMetPro 41
Db      61 TGCAGGCTTCTGGATACACCTTCACCTGAGTATGTTATTCCTGGGTAAAGAGACCT 120
Qy      42 GlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyrSer 61
Db      121 GGACAGGCTTCAAGGCTGAGTGAAGATTATTCCTGGAAGTGGTAGTACTTCTTCAAT 180
Qy      62 ProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyrLeu 81
Db      181 GAAATTCAGAGGCGCAAGCGCAATCATCTGCTGACAAATCCACTAACACAGCCTTACAT 240
Qy      82 GlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAspVal 101
Db      241 GAGCTCAGACAGCTTGAATCTGAGACACACTGCGCTTCTATTCTGTACAAAGAGAGATCTT 300
Qy      102 GlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 121
Db      301 GGG-----GGCCAA 309
Qy      122 GlyThrLeuValThrValSerSer 129
Db      310 GGGTCTGTGCTGACCGTCTTCTCA 333

```

RESULT 13

```

US-11-221-902-83
; Sequence 83, Application US/11221902
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGA
; FILE REFERENCE: 040000-031285
; CURRENT APPLICATION NUMBER: US/11/221,902
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 83
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(360)
; FEATURE:
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
; OTHER INFORMATION: sequences
US-11-221-902-83

```

Alignment Scores:

```

Pred. No.: 4 72e-34 Length: 360
Score: 361.50 Matches: 72
Percent Similarity: 72.1% Conservative: 21
Best Local Similarity: 55.8% Mismatches: 27
Query Match: 51.6% Indels: 9
DB: 7 Gaps: 2

```

US-10-092-640-32 (1-129) x US-11-221-902-83 (1-360)

```

Qy      1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
Db      1 CAGGTCCAGGCTTCTGGATACACCTTCACCTGAGTGAAGAGAGCCCTGAGTGAAGAGG 60
Qy      21 SerCyAlsyGlySerGlyTyrSerPheThrSerTyrTriPleAlaTrpValArgGlnMet 40
Db      61 TCCTGCAAGGCTTCTGGATACACCTTCACCTGAGTGAAGAGAGCCCTGAGTGAAGAGG 120
Qy      41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
Db      121 CCCGACAGGCGCTTGAATGGAGTGAAGCTTAAATTCCTAACAAATGAGTGTCTCTCAG 180
Qy      61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
Db      181 AACCAAGAAATTCAGAGACCGGCTGACATCTGCGACACTCCACCTCCACAGGCTTAC 240
Qy      81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100

```

```
Db      241 ATGAGACTCTCTCTCTGCGCTCTGAGGACACCGCGCTATTACTGTGACGCC----- 294
      101 VALGIYTYrCySerSerSerSernCysAlaIySTrPProGIuTYrPheGlnHisTrpGIY 120
      295 -----TCCACTATGATTACCAACTAT-----GTTATGAGCTACTGTGGGT 333
QY      121 GInGIYThrLeuValThrValSerSer 129
      334 CAAGGACCCCTGCTCAGCGCTCTCTCA 360
RESULT 14
US-11-297-317-12
; Sequence 12, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballedo Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce W. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Nucleotide sequence encoding amino acid sequence SEQ ID NO:10
US-11-297-317-12
Alignment Scores:
Pred. No.: 1.03e-33 Length: 354
Score: 358.50 Matches: 69
Percent Similarity: 72.1% Conservative: 24
Best Local Similarity: 53.5% Mismatches: 25
Query Match: 51.2% Indels: 11
Gaps: 2
DB:
US-10-092-640-32 (1-129) x US-11-297-317-12 (1-354)
QY      1 GInValGInLeuLeuGInSerGIyAlaGIuLeuLySlySProGIyGluSerLeuLySile 20
      1 CAGGTGCACTGCTGTGAGTCAAGAGCGAAGTGAAGAAACCTGGGCTTCAGTGAAGTG 60
Db      21 SerCySlySGlySerGIyTYrSerPheThrSerTYrTPiLeAlaTrpValArgGlnMet 40
      61 TCCTGCAAGGCGCTCTGATACACATTCCTAATTATATATTCACACTGGGTGAAGCAGAG 120
Db      41 ProGIySGlyLeuGIuTYrMetGIyLeuIleTYrProGIyAspSerAspThrLySTYr 60
      121 CTTGTCAGGCGCTTGAATGATGATTTTAACTTCTTACATATGATGATGATGATGATC 180
QY      61 SerProSerPheGlnGIyGInValThrIleSerValAspLySerValSerThraIaTYr 80
      181 AATGAGAGTTCAAGGACGAGGCGCACATCACTGCAAAACAATCCATCAGCAGAGCTTAC 240
Db      81 LeuGInTrpSerSerLeuLySProSerAspSerAlaValTYrPheCysAlaArgHisasp 100
      241 ATGAGACTCAGCAGCTGCGCTCTGAGGACACTGCGCTCTACTACTGTCACAGA----- 294
QY      101 VALGIYTYrCySerSerSerSernCysAlaIySTrPProGIuTYrPheGlnHisTrpGIY 120
      295 -----TCAGGACCCCTATGCTCG-----TTGACACCTGGGCG 327
Db      121 GInGIYThrLeuValThrValSerSer 129
      |||||
      |||||
      |||||
```

```
Db      328 CAAGGACCAACGCGTCAACCGTCTCTCA 354
RESULT 15
US-11-297-317-15
; Sequence 15, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballedo Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce W. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 8687
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCV-HuB-VHQ
; OTHER INFORMATION: (Complete DNA Sequence of a humanised heavy chain expression vect
US-11-297-317-15
Alignment Scores:
Pred. No.: 8.23e-32 Length: 8687
Score: 358.50 Matches: 69
Percent Similarity: 72.1% Conservative: 24
Best Local Similarity: 53.5% Mismatches: 25
Query Match: 51.2% Indels: 11
Gaps: 2
DB:
US-10-092-640-32 (1-129) x US-11-297-317-15 (1-8687)
QY      1 GInValGInLeuLeuGInSerGIyAlaGIuLeuLySlySProGIyGluSerLeuLySile 20
      3921 CAGGTGCACTGCTGTGAGTCAAGAGCGAAGTGAAGAAACCTGGGCTTCAGTGAAGTG 3980
Db      21 SerCySlySGlySerGIyTYrSerPheThrSerTYrTPiLeAlaTrpValArgGlnMet 40
      3981 TCCTGCAAGGCGCTCTGATACACATTCCTAATTATATATTCACACTGGGTGAAGCAGAG 4040
QY      41 ProGIySGlyLeuGIuTYrMetGIyLeuIleTYrProGIyAspSerAspThrLySTYr 60
      4041 CCTGTCAGGCGCTTGAATGATGATTTTAACTTCTTACATCATGATGATGATGATGATC 4100
Db      61 SerProSerPheGlnGIyGInValThrIleSerValAspLySerValSerThraIaTYr 80
      4101 AATGAGAGTTCAAGGACGAGGCGCACACTCACTGCAAAACAATCCATCAGCAGACCTTAC 4160
QY      81 LeuGInTrpSerSerLeuLySProSerAspSerAlaValTYrPheCysAlaArgHisasp 100
      4161 ATGAGACTCAGCAGCTGCGCTCTGAGGACACTGCGCTCTACTACTGTCACAGA----- 4214
Db      101 VALGIYTYrCySerSerSerSernCysAlaIySTrPProGIuTYrPheGlnHisTrpGIY 120
      4215 -----TCAGGACCCCTATGCTCG-----TTGACACCTGGGCG 4247
QY      121 GInGIYThrLeuValThrValSerSer 129
      4248 CAAGGACCAACGCGTCAACCGTCTCTCA 4274
Search completed: May 25, 2006, 21:28:38
Job time : 25.425 secs
```

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:11:24 ; Search time 4225.86 Seconds
(without alignments)
2519.544 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588
Sequence: 1 GSVLTGPPPSVSAARQKVTI.....WDSLSGWRVGGSTKLTVLG 111

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=xlh
-Q/abs/ABSSWB.spool/US10092640/runat_25052006_155713_5836/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORH=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs05h
-USER=US10092640.@CCN_1_1_5767_@runat_25052006_155713_5836 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:.*
1: gb_env:.*
2: gb_pat:.*
3: gb_ph:.*
4: gb_pl:.*
5: gb_pr:.*
6: gb_ro:.*
7: gb_sts:.*
8: gb_sy:.*
9: gb_un:.*
10: gb_vi:.*
11: gb_ov:.*
12: gb_hvg:.*
13: gb_in:.*
14: gb_cm:.*
15: gb_ba:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588	100.0	333	5 HSU36541	U36541 Human anti-
2	588	100.0	333	5 HSU38338	U38338 Human anti-
3	588	100.0	774	2 AR083879	AR083879 Sequence

4	588	100.0	774	2	AR278815	AR278815 Sequence
5	588	100.0	1509	8	AF516873	AF516873 Synthetic
6	580	98.6	333	5	HSU38345	U38345 Human anti-
7	579	98.5	333	5	HSU38342	U38342 Human anti-
8	578	98.3	333	5	HSU38346	U38346 Human anti-
9	575	97.8	333	5	HSU38335	U38335 Human anti-
10	573	97.4	333	5	HSU38341	U38341 Human anti-
11	569	96.8	333	5	HSU38336	U38336 Human anti-
12	568	96.6	333	5	HSU38343	U38343 Human anti-
13	567	96.4	333	5	HSU38347	U38347 Human anti-
14	562	95.6	333	5	HSU38340	U38340 Human anti-
15	558	94.9	333	5	HSU38344	U38344 Human anti-
16	556	94.6	333	5	HSU38337	U38337 Human anti-
17	556	94.6	342	5	HSU38376	HSU38376 Human anti-
18	542.5	92.3	336	5	HSU36537	HSU36537 Human anti-
19	536	91.2	333	5	HSU36538	HSU36538 Human anti-
20	536	91.2	333	5	HSU38339	HSU38339 Human anti-
21	535	91.0	333	5	HSU36536	HSU36536 Human anti-
22	527	89.6	387	5	HSU36536	HSU36536 Human anti-
23	527	89.6	816	5	AB064150	AB064150 Homo sapi
24	526	89.5	781	5	AB064216	AB064216 Homo sapi
25	525	89.3	333	5	HSU36540	HSU36540 Human anti-
26	523	88.9	744	8	AF487502	AF487502 Synthetic
27	523	88.9	333	5	HSU36539	HSU36539 Human anti-
28	522	88.8	331	5	DO187610	DO187610 Homo sapi
29	521	88.6	750	8	DO250251	DO250251 Synthetic
30	518	88.1	732	2	CO859620	CO859620 Sequence
31	517	87.9	744	8	AF487503	AF487503 Synthetic
32	517	87.9	744	8	CO832205	CO832205 Sequence
33	516	87.8	744	8	AF487505	AF487505 Synthetic
34	516	87.8	790	5	AB064206	AB064206 Homo sapi
35	516	87.8	831	5	AB064224	AB064224 Homo sapi
36	516	87.8	908	2	AR366275	AR366275 Sequence
37	516	87.7	729	8	DO250225	DO250225 Synthetic
38	515.5	87.7	342	5	HSU36539	HSU36539 Homo sapi
39	515	87.6	706	2	CO832195	CO832195 Sequence
40	514	87.4	744	8	DO201312	DO201312 Synthetic
41	514	87.4	744	8	AF487508	AF487508 Synthetic
42	514	87.4	744	8	AF487508	AF487508 Synthetic
43	514	87.4	744	8	AF487508	AF487508 Synthetic
44	514	87.4	744	8	AF487508	AF487508 Synthetic
45	514	87.4	744	8	AF487509	AF487509 Synthetic

ALIGNMENTS

RESULT 1
HSU36541
LOCUS
DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V region mRNA,
partial cds.
U36541
U36541.1 GI:1145221
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 333)
Schier R., Bye J., Apell G., McCall A., Adams G.P., Weiner L.M. and
Marks J.D.
Isolation of high affinity monomeric Human anti-c-erbB-2 single
chain Fv using affinity driven selection
J. Mol. Biol. (1995) In press
2 (bases 1 to 333)
Schier R.
Direct Submission
Submitted (18-SEP-1995) Robert Schier, Anesthesia, University of
California at San Francisco, 1001 Potrero Avenue, San Francisco, CA
94110, USA
JOURNAL
TITLES
REFERENCE
FEATURES
source
1. .333

Alignment Scores:

Pred. No.: 1 94e-54 Length: 774
 Score: 588.00 Matches: 111
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x AR083879 (1-774)

QY 1 GlnSerValleuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20

Db 433 CAGTCTGTGTGAAGCGAGCCGCTCAGTCTCGCGGCCCGACAGAGAGGTCACCATC 492

QY 21 SerCysSerGlySerSerSerSerAniIleGlyAsnAsnTrpValSerTrpTrpGlnGlnIleu 40

Db 493 TCTGCTCTGGAGAGCAGCTCCAACTGGGAATTAATGATCTCTGTCAGCAGCAGCTC 552

QY 41 ProGlyThrAlaProIysIleuIleTyrglyHisThrAsnArgProIleGlyValPro 60

Db 553 CCGAGAACAGCCCCCAACTCCTCATCTATGTGCACCAATCGGCCCGAGGGGTCCTC 612

QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

Db 613 GACCGATTCTCTGGCTCCAAGTCTGGACCTCGCTCCCTGSCCATCAGTGGGTTCCGG 672

QY 81 SerGluAspGluAlaAspTrpTrpCysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100

Db 673 TCCGAGATGAGCGCTGATTAATTAATCTGTGCAGCATGGAGATGACAGCTGAGTGGGTG 732

QY 101 PheGlyGlyGlyThrIysLeuThrValIleuGly 111

Db 733 TTGGCGGAGGAGCAAGCTGACCGTCTTAGGT 765

RESULT 4 AR278815 774 bp DNA linear PAT 10-APR-2003

LOCUS Sequence 4 from patent US 6512097.

ACCESSION AR278815

VERSION AR278815.1 GI:29713203

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 1 94e-54 Length: 774

Score: 588.00 Matches: 111

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

QY 41 ProGlyThrAlaProIysIleuIleTyrglyHisThrAsnArgProIleGlyValPro 60

Db 553 CCGAGAACAGCCCCCAACTCCTCATCTATGTGCACCAATCGGCCCGAGGGGTCCTC 612

QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

Db 613 GACCGATTCTCTGGCTCCAAGTCTGGACCTCGCTCCCTGSCCATCAGTGGGTTCCGG 672

QY 81 SerGluAspGluAlaAspTrpTrpCysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100

Db 673 TCCGAGATGAGCGCTGATTAATTAATCTGTGCAGCATGGAGATGACAGCTGAGTGGGTG 732

QY 101 PheGlyGlyGlyThrIysLeuThrValIleuGly 111

Db 733 TTGGCGGAGGAGCAAGCTGACCGTCTTAGGT 765

RESULT 5 AF516873 1509 bp mRNA linear SYN 01-MAR-2004

LOCUS AF516873 Synthetic construct membrane-acting immunotoxin fusion protein

DEFINITION AF516873 mRNA, complete cds.

ACCESSION AF516873.1 GI:31324248

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 1509)

2 (bases 1 to 1509)

3 (bases 1 to 1509)

4 (bases 1 to 1509)

5 (bases 1 to 1509)

6 (bases 1 to 1509)

7 (bases 1 to 1509)

8 (bases 1 to 1509)

9 (bases 1 to 1509)

10 (bases 1 to 1509)

11 (bases 1 to 1509)

12 (bases 1 to 1509)

13 (bases 1 to 1509)

14 (bases 1 to 1509)

15 (bases 1 to 1509)

16 (bases 1 to 1509)

17 (bases 1 to 1509)

18 (bases 1 to 1509)

19 (bases 1 to 1509)

20 (bases 1 to 1509)

21 (bases 1 to 1509)

22 (bases 1 to 1509)

23 (bases 1 to 1509)

24 (bases 1 to 1509)

25 (bases 1 to 1509)

26 (bases 1 to 1509)

27 (bases 1 to 1509)

28 (bases 1 to 1509)

29 (bases 1 to 1509)

30 (bases 1 to 1509)

31 (bases 1 to 1509)

32 (bases 1 to 1509)

33 (bases 1 to 1509)

34 (bases 1 to 1509)

35 (bases 1 to 1509)

36 (bases 1 to 1509)

```

/product="membrane-acting immunotoxin fusion protein"
/protein_id="AAP47198.1"
/db_xref="GI:31324249"
/translation="MSQVQLDLSGAEVKKPKGESLKISCKSGSYSTSYIAMIWROMPG
KGLRYMGLIYPGSDITKYSPSFOGVITISVDKSVSTAYLQWMSLKPSDAVYFCARH
VGYCSNCAKMEYFOHMGQGLTVLTVSGSGSGSGSGSGLTQPSVGAAP
GOKVTISCSGSSNIGNNVSWYQOLPGPAPLLIYGHTRPAGVDRDRSGSGTSA
SLAISGPRSEDEADYCAAMDLSLGMVGGGCTKLVLGIESGGSGSGSGSGSGSP
RSLDNPNTVPYVQYINQALHLMNAPOGADIDPILNPNFEKALQIANGTENSATV
TLNQSVIQOTVLSVWEDQKTIQIEVLALVNTSFMNSVETIKGTFTNLDTQIDE
AMIFWHSLSAHTSYNYNLIPLFSIQNEIDCAVNAVLPLAEVSDVEKQVLPFTIKDS
ARVEYMKALTLVQALHSSNAPIVDIIFLEQKLISEDLNSAVDHHHHH"
misc_feature
787..834
/note="serine/glycine linker"

```

ORIGIN

Alignment Scores:

```

Pred. No.: 4,64e-54 Length: 1509
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

```

US-10-092-640-36 (1-111) x AFS16873 (1-1509)

OY 1 GlnSerValLeuThGlnProSerValSerAlaAlaProGlyGlnIysValThrIle 20

DB 448 CAGTCTGTTGTTACGAGCGCCCTCAGTCTGCGGCCCCAGAGAGAAAGTCAACATC 507

OY 21 SerCysSerGlySerSerSerSerAniIleGlyAsnaSenTyValSerTyrPyrGlnGlnLeu 40

DB 508 TCTCTGCTCGGAAGACGCTCCAACTGGGAATTAATGATCTCTGGTAACAGCAGCTC 567

OY 41 ProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60

DB 568 CCAGGAACAGCCCCCAACTCTCATCTATGATGTCACACCAATCGGCCCCAGAGGGTCCCT 627

OY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

DB 628 GACCATTTCTGCTGCCAAGTCTGGCACCCTCAGCTCCCTGCGCATCGTGGTTCGG 687

OY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTTPAspAspSerLeuSerGlyTyrVal 100

DB 668 TCCGAGGATGAGGCTGATTATTACTGTGACGATGGAGTACGACCTGTGTTGGGTG 747

OY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111

DB 748 TTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 780

RESULT 6

LOCUS HSU38345

DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,

ACCESSION U38345

VERSION U38345.1

KEYWORDS GI:1145351

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 333)

AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.

TITLE Identification of functional and structural amino-acid residues by

JOURNAL Gene 169 (2), 147-155 (1996)

REFERENCE 2 (bases 1 to 333)

AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.

```

TITLE Direct Submission
JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
source
1..333
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C6PM11"
/clone_11b="semisynthetic scFv phage display library"
<1..>333
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin light chain V"
/protein_id="AAB09655.1"
/db_xref="GI:1145352"
/translation="QSVLTQPPSVSAARQAVTISCSGSSNIGSNVSWYQOLPGTA
PKLLIYGHTRPAGVDRDRSGSGSGTSAISLISGRSEDEADYCAAMDALSGWVFG
GTXKLTVLG"

```

CDS

ORIGIN

Alignment Scores:

```

Pred. No.: 4.83e-54 Length: 333
Score: 580.00 Matches: 109
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.2% Mismatches: 0
Query Match: 98.6% Indels: 0
DB: 5 Gaps: 0

```

US-10-092-640-36 (1-111) x HSU38345 (1-333)

OY 1 GlnSerValLeuThGlnProSerValSerAlaAlaProGlyGlnIysValThrIle 20

DB 1 CAGTCTGTTGTTACGAGCGCCCTCAGTCTGCGGCCCCAGAGAGAAAGTCAACATC 60

OY 21 SerCysSerGlySerSerSerSerAniIleGlyAsnaSenTyValSerTyrPyrGlnGlnLeu 40

DB 61 TCTCTGCTCGGAAGACGCTCCAACTGGGAATTAATGATCTCTGGTAACAGCAGCTC 120

OY 41 ProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60

DB 121 CCAGGAACAGCCCCCAACTCTCATCTATGATGTCACACCAATCGGCCCCAGAGGGTCCCT 180

OY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

DB 181 GACCATTTCTGCTGCCAAGTCTGGCACCCTCAGCTCCCTGCGCATCGTGGTTCGG 240

OY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTTPAspAspSerLeuSerGlyTyrVal 100

DB 241 TCCGAGGATGAGGCTGATTATTACTGTGACGATGGAGTACGACCTGTGTTGGGTG 300

OY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111

DB 301 TTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 333

RESULT 7

LOCUS HSU38342

DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,

ACCESSION U38342

VERSION U38342.1

KEYWORDS GI:1145345

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 333)

AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.

TITLE Identification of functional and structural amino-acid residues by

JOURNAL Gene 169 (2), 147-155 (1996)

PUBMED 8647439
 REFERENCE 2 (bases 1 to 333)
 AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
 TITLE Direct Submission
 JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES
 source
 1..333
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_11b="semisynthetic scfv phage display library"
 <1..>333
 /codon_start=1
 /product="anti-c-erbB-2 immunoglobulin light chain v"
 /protein_id="AB09652.1"
 /db_xref="GI:1145346"
 /translation="QSVLTQPPSVSAAPGOKTISGFGSSSNIGNNVSWYQOLPGTA PKLIIQHTNRPAGVDPDRSGSKSGTSASLISGFRSEDEADYICAMDESLSGWVFG GGTKLTVLG"

ORIGIN
 Alignment Scores:
 Pred. No.: 6,21e-54 Length: 333
 Score: 579.00 Matches: 110
 Percent Similarity: 99.1% Conservative: 0
 Best Local Similarity: 99.1% Mismatches: 1
 Query Match: 98.5% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-36 (1-111) x HSU38342 (1-333)

QY 1 GlnSerValleuthrGlnProSerValSerAlaProGlyGlnIysValThrIle 20
 Db 1 CAGTCTGTGTGACGACGCCCTCAGTCTCGCGCCCAAGACAGAAAGTCACCATC 60
 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
 Db 61 TCCTGCTGTGAGAGAGCTCAACATGTAATATATATATATATATATATATATATAT 120
 QY 41 ProGlyThrAlaProIysLeuLeuIleTyrglyHisThrAsnArgProAlaGlyValPro 60
 Db 121 CCAAGAACAGCCCCCAAACTCTCATCTATGTCACACCAATCGCCCGAGGGTCCCT 180
 QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 181 GACCGATTCTCTGGCTCCAAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGGTTCCGG 240
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaITrPAspAspSerLeuSerGlyTyrPval 100
 Db 241 TCCGAGATGAGGCGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
 QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
 Db 301 TTCGGCGAGGAGGACCAAGCTGACCGTCTAAGT 333

RESULT 8
 HSU38346 333 bp mRNA linear PRI 02-OCT-1996
 LOCUS Human anti-c-erbB-2 immunoglobulin light chain v mRNA, partial cds,
 DEFINITION clone C6PM12.
 ACCESSION U38346.1 GI:1145353
 VERSION U38346.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 333)
 AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and

Markes,J.D.
 TITLE Identification of functional and structural amino-acid residues by
 JOURNAL parsimonious mutagenesis
 PUBMED Gene 169 (2), 147-155 (1996)
 REFERENCE 8647439
 AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
 TITLE Direct Submission
 JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES
 source
 1..333
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C6PM12"
 /clone_11b="semisynthetic scfv phage display library"
 <1..>333
 /codon_start=1
 /product="anti-c-erbB-2 immunoglobulin light chain v"
 /protein_id="AB09656.1"
 /db_xref="GI:1145354"
 /translation="QSVLTQPPSVSAAPGOKTISGFGSSSNIGNNVSWYQOLPGTA PKLIIQHTNRPAGVDPDRSGSKSGTSASLISGFRSEDEADYICAMDESLSGWVFG GGTKLTVLG"

ORIGIN
 Alignment Scores:
 Pred. No.: 7.98e-54 Length: 333
 Score: 578.00 Matches: 109
 Percent Similarity: 99.1% Conservative: 1
 Best Local Similarity: 98.2% Mismatches: 1
 Query Match: 98.3% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-36 (1-111) x HSU38346 (1-333)

QY 1 GlnSerValleuthrGlnProSerValSerAlaProGlyGlnIysValThrIle 20
 Db 1 CAGTCTGTGTGACGACGCCCTCAGTCTCGCGCCCAAGACAGAAAGTCACCATC 60
 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
 Db 61 TCCTGCTGTGAGAGAGCTCAACATGTAATATATATATATATATATATATATATAT 120
 QY 41 ProGlyThrAlaProIysLeuLeuIleTyrglyHisThrAsnArgProAlaGlyValPro 60
 Db 121 CCAAGAACAGCCCCCAAACTCTCATCTATGTCACACCAATCGCCCGAGGGTCCCT 180
 QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 181 GACCGATTCTCTGGCTCCAAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGGTTCCGG 240
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaITrPAspAspSerLeuSerGlyTyrPval 100
 Db 241 TCCGAGATGAGGCGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
 QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
 Db 301 TTCGGCGAGGAGGACCAAGCTGACCGTCTAAGT 333

RESULT 9
 HSU38335 333 bp mRNA linear PRI 02-OCT-1996
 LOCUS Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
 DEFINITION clone C6PM1.
 ACCESSION U38335.1 GI:1145331
 VERSION U38335.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo

AUTHORS 1 (bases 1 to 333)

TITLE Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.

JOURNAL Identification of functional and structural amino-acid residues by parsimonious mutagenesis

PUBMED Gene 169 (2), 147-155 (1996)

8647439

REFERENCE 2 (bases 1 to 333)

AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES

source

1..333

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="C6PM1"

/clone_1ib="seemisynthetic scfv phage display library"

<1..>333

/codon_start=1

/product="anti-C-erbB-2 immunoglobulin light chain V"

/protein_id="AAB09645.1"

/db_xref="GI:1145332"

/translation="OSVLTOPPSVSAARGKVTISGSGSSNMNNVSWYQQLPGRPAKLIVGHTRNPAGVPDRFSSKSGTASLASISFRBEDADYICAMDDTLSSWVFGGTRKLTIVIG"

ORIGIN

Alignment Scores:

Pred. No.: 1.7e-53 Length: 333

Score: 575.00 Matches: 108

Percent Similarity: 99.1% Conservative: 2

Best Local Similarity: 97.3% Mismatches: 1

Query Match: 97.8% Indels: 0

DB: Gaps: 5

US-10-092-640-36 (1-111) x HSU38335 (1-333)

QY 1 GlnSerValLeuThrInGInProSerSerValSerAlaAlaProGlyGlnIysValThrIle 20

Db 1 CAGTCTGTGTGACGACGACCGCCCTCACTGTCTGGCGCCACAGACAGAGTCAACATC 60

QY 21 SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnIleu 40

Db 61 TCCGCTCTGGAGAGAGCTCCACACATGATATATATATATGATCTGTGTACACAGCTC 120

QY 41 ProGlyThrAlaProGlySleuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60

Db 121 CCAGAAACAGCCCCCAAACTCCTCATCTATATGTCACACAAATCGGCCGCGAGGGGTCCCT 180

QY 61 AsparGPheserGlySerTyrSerGlyThrSerIAserLeuAlaIleSerGlyPheArg 80

Db 181 GACCGATTCTGTGGCTCCAAAGTCGTGGACCTCAAGCTCCTCGGCCCATAGTGGTTCGG 240

QY 81 SerGlnAspGlnAlaAspTyrTyrCysAlaAlaIleTyrAspAspSerLeuSerGlyTyrVal 100

Db 241 TCCGAGATGAGGCTGATTATTACTGTGCACACATGGATGATACTTGTCTGTGGGTG 300

QY 101 PheGlyGlyGlyTThrIysLeuThrValIleuGly 111

Db 301 TTCGGCGGAGGAGACCAAGCTGACCGTCTCAAGT 333

RESULT 10

LOCUS HSU38341 333 bp mRNA linear PRI 02-OCT-1996

DEFINITION Human anti-C-erbB-2 immunoglobulin light chain V mRNA, partial cds,

clone C6PM1.

FEATURES

ORIGIN

US38341.1 GI:1145343

KEYWORDS	Homo sapiens (human)
SOURCE ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae; Homo.
REFERENCE AUTHORS	1 (bases 1 to 333) Schier,J.D., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
TITLE	Identification of functional and structural amino-acid residues by parsimonious mutagenesis
JOURNAL	Gene 169 (2), 147-155 (1996)
PUBMED	8647439
REFERENCE AUTHORS	2 (bases 1 to 333) Schier,J.D., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.
TITLE	Direct Submission
JOURNAL	Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES	Location/Qualifiers
source	1..333 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="C6PM7" /clone_id="semsynthetic scfv phage display library" <1..>333 /codon_start=1 /product="anti-C-erbB-2 immunoglobulin light chain v" /protein_id="AAB09651.1" /db_xref="GI:1145344" /translation="QSVLTQPSPVSAAPGKVTISCGSSSNIGNNVSVYQQLPGTA PKLIIGRTNRPAVGPDPRFSGSKGSITSASIALISGFSEDEADYVCAAMDLSLGWFG GGTFLVLGG"
CDS	
ORIGIN	
Alignment Scores:	
Pred. No.:	2,81e-53 Length: 333
Score:	573.00 Matches: 109
Percent Similarity:	98.2% Conservative: 0
Best Local Similarity:	98.2% Mismatches: 2
Query Match:	97.4% Indels: 0
DB:	Gaps: 0
US-10-092-640-36 (1-111) x HSU38336 (1-333)	
Oy	1 GlnserValIeuThrGInPProSerSeValSerAlaIalProGlyGInLysValThrIle 20
Dd	1 CAGTCtGTgTGAAGcAGcCGCCcCTCAgTGTcCGGCCcCACAgAcAGAAgGTACCATC 60
Oy	21 SerCySergLySerSerSerAsnIlGlyAsnAsnTyValSerTrPTyrGInGInLeu 40
Dd	21 TCCTGCCTCTGGAAcACACTCCAAcATTGGTAATATATATATCTTGTTACcAGcACACTC 120
Oy	41 ProGlyThrAlaPolylsLeuLeuIleTYrGLyHisThrAsnArgProAlaGlyValPro 60
Dd	121 CCAGAACAAGCCCCCAAACCTCTCATATTAGTGTGcACCAATGGcCCCGAGggGTCCT 180
Oy	61 AspargheserGlySerlysSergLyThSerAlaSerLeuAlaIleSergLyPhearg 80
Dd	181 GACCGATTCTCTGTGCTCCAAGTGTGGACCTCAgcCTCCCTGGCCATCAAGTGGGTTCCGG 240
Oy	81 SerGluaSpGluAlaAspyTYrCYAlaAlaITrpAspaSpSerLeuSergLyTrpVal 100
Dd	241 TCCAGAGATAGAGCTGTATTATTACTGTGcAGCAGcAGGATCATTTCTGTGTGGTGGTG 300
Oy	101 PheGlyGlyGlyThrLysLeuThValleGly 111
Dd	301 TTCCGGCGAGGAGACCAAGCTGACCGCTCTTAGT 333
RESULT 11	
LOCUS	HSU38336 333 bp mRNA linear PRI 02-OCT-1996

DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
clone C6PM2.

ACCESSION U38336

VERSION U38336.1 GI:1145333

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 333)
Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis

JOURNAL Gene 169 (2), 147-155 (1996)

PUBMED 8647439

REFERENCE 2 (bases 1 to 333)
Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES
source location/Qualifiers
1..333
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C6PM2"
/clone_lib="semisynthetic scFv phage display library"
<1..>333
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin light chain V"
/protein_id="AAB09646.1"
/db_xref="GI:1145334"
/translation="OSVLTQPPSVSAAPGOKVTISCGSSSNIGKNVSWYQOLPQTA
PKLIYGHANRPAGVDRFRSGSKTSASLAIISGFRSEBDADYCAAMDSDSYSGWVFG
GGTKLTVLG"

CDS
1..>333
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin light chain V"
/protein_id="AAB09646.1"
/db_xref="GI:1145334"
/translation="OSVLTQPPSVSAAPGOKVTISCGSSSNIGKNVSWYQOLPQTA
PKLIYGHANRPAGVDRFRSGSKTSASLAIISGFRSEBDADYCAAMDSDSYSGWVFG
GGTKLTVLG"

ORIGIN

Alignment Scores:

Pred. No.:	7,686-53	Length:	333
Score:	569.00	Matches:	107
Percent Similarity:	98.2%	Conservative:	2
Best Local Similarity:	96.4%	Mismatches:	2
Query Match:	96.8%	Indels:	0
DB:	5	Gaps:	0

US-10-092-640-36 (1-111) x HSU38336 (1-333)

QY 1 GlnSeValleuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
1 CAGTCTGTGTGACGACGCGCCCTCAGTCTGCGGCCCAAGACAGAGTCAACATC 60
DB 1 CAGTCTGTGTGACGACGCGCCCTCAGTCTGCGGCCCAAGACAGAGTCAACATC 60

QY 21 SerCySeSerGlySerSerSerAenIleGlyAenAsnTyValSerTPYrGlnGlnIleu 40
61 TCTGTCTCTGGAAGCGCTCCCAATGTAAGATTATGATCTCGTAACGACGAGCTC 120

QY 41 ProGlyThrAlaProIleuLeuIleTyGlyHisThrAsnArgProIleGlyValPro 60
121 CCAAGAAACGCCCAACTCCTCATCTATGTCACACCAATGCGCCCGAGGGGTCCT 180

QY 61 AppaArgPheSerGlySerIleuLeuIleTyGlyHisThrAsnArgProIleGlyValPro 80
181 GACCGATTCTCTGCTCCCAAGTCTGACCTCAGCTCCCTGCGCATCAGTGGTCCG 240

QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTrpAspAspSerIleuSerGlyTrpVal 100
241 TCCGAGGATGAGGCTATTATTAATCTGTCGACGATGGAGTACGTCGTGACTGGTGGGTC 300

QY 101 PheGlyGlyGlyThrIleuLeuValIleuGly 111
301 TTCGCGGAGGAGGACCAAGCTGACGCTCTAAGT 333

DB

RESULT 12
HSU38343
LOCUS 333 bp mRNA linear PRI 02-OCT-1996

DEFINITION Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
clone C6PM9.

ACCESSION U38343

VERSION U38343.1 GI:1145347

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 333)
Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis

JOURNAL Gene 169 (2), 147-155 (1996)

PUBMED 8647439

REFERENCE 2 (bases 1 to 333)
Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES
source location/Qualifiers
1..333
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C6PM9"
/clone_lib="semisynthetic scFv phage display library"
<1..>333
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin light chain V"
/protein_id="AAB09653.1"
/db_xref="GI:1145348"
/translation="OSVLTQPPSVSAAPGOKVTISCGSSSNIGKNVSWYQOLPQTA
PKLIYGHANRPAGVDRFRSGSKTSASLAIISGFRSEBDADYCAAMDSDSYSGWVFG
GGTKLTVLG"

CDS
1..>333
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin light chain V"
/protein_id="AAB09653.1"
/db_xref="GI:1145348"
/translation="OSVLTQPPSVSAAPGOKVTISCGSSSNIGKNVSWYQOLPQTA
PKLIYGHANRPAGVDRFRSGSKTSASLAIISGFRSEBDADYCAAMDSDSYSGWVFG
GGTKLTVLG"

ORIGIN

Alignment Scores:

Pred. No.:	9,886-53	Length:	333
Score:	568.00	Matches:	107
Percent Similarity:	97.3%	Conservative:	1
Best Local Similarity:	96.4%	Mismatches:	3
Query Match:	96.6%	Indels:	0
DB:	5	Gaps:	0

US-10-092-640-36 (1-111) x HSU38343 (1-333)

QY 1 GlnSeValleuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
1 CAGTCTGTGTGACGACGCGCCCTCAGTCTGCGGCCCAAGACAGAGTCAACATC 60
DB 1 CAGTCTGTGTGACGACGCGCCCTCAGTCTGCGGCCCAAGACAGAGTCAACATC 60

QY 21 SerCySeSerGlySerSerSerAenIleGlyAenAsnTyValSerTPYrGlnGlnIleu 40
61 TCTGTCTCTGGAAGCGCTCCCAATGTAAGATTATGATCTCGTAACGACGAGCTC 120

QY 41 ProGlyThrAlaProIleuLeuIleTyGlyHisThrAsnArgProIleGlyValPro 60
121 CCAAGAAACGCCCAACTCCTCATCTATGTCACACCAATGCGCCCGAGGGGTCCT 180

QY 61 AppaArgPheSerGlySerIleuLeuIleTyGlyHisThrAsnArgProIleGlyValPro 80
181 GACCGATTCTCTGCTCCCAAGTCTGACCTCAGCTCCCTGCGCATCAGTGGTCCG 240

QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTrpAspAspSerIleuSerGlyTrpVal 100
241 TCCGAGGATGAGGCTATTATTAATCTGTCGACGATGGAGTACATTCTATTCTGTTGGGTC 300

DB

Oy	101	PheGlyGlyGlyYThrValLeuThrValIleGly	111
Db	301	TTGGCGGAGGACCAAGCTACGCTCTAGGT	333
RESULT 13			
LOCUS	HSU38347	333 bp	mRNA
DEFINITION	Human anti-C-erbB-2 immunoglobulin light chain V mRNA, partial cds,		
ACCESSION	U38347		
VERSION	U38347.1	GI:1145355	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 333) Schlier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.		
TITLE	Identification of functional and structural amino-acid residues by		
JOURNAL	paralmonous mutagenesis		
PUBMED	Gene 169 (2), 147-155 (1996)		
REFERENCE	8647439		
AUTHORS	2 (bases 1 to 333) Schlier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and Marks,J.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-OCT-1995) Robert Schlier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA		
FEATURES	Location/Qualifiers		
source	1..333 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="C6PM13" /clone_lib="semisynthetic scfv phage display library" 1..>333 /codon_start=1 /product="anti-C-erbB-2 immunoglobulin light chain V" /protein_id="AAB09657.1" /db_xref="GI:1145356" /translation="OSVLTQPPSYSAAPGOKVTWSCSSSSNIGKNVSWYQQLPGRPA PKLIYGHTRNRPAGVDPDRFSSKSGKTSALISGRSRDEADYVCAAMDYLSGWTG GGRLLTVLG"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.27e-52	Length:	333
Score:	567.00	Matches:	107
Percent Similarity:	98.2%	Conservative:	2
Best Local Similarity:	96.4%	Mismatches:	0
Query Match:	96.4%	Indels:	0
DB:	5	Gaps:	0
US-10-092-640-36 (1-111) x HSU38347 (1-333)			
Oy	1	GLNSERVALLLEuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle	20
Db	1	CAGTCTGTTGACCGCACCGCCCTCATGTCTGGGCCCCAGGACAGAAAGTCACATG	60
Oy	21	SeRCysSerGlySerSerSerSerAsnIleGlyAsnAsnValSerTyrGlnGlnLeu	40
Db	61	TCCTGCTCTGAAAGACGCTCCAACTTGTGTAATAATTTCGATCTCTGATACAGCAGCTC	120
Oy	41	ProGlyThrAlaProIleValLeuLeuIleTyrGlyIshThrAsnArgProAlaGlyValPro	60
Db	121	CCAGGAACAGCCCCCAAACTCCTCATATGATGTCACACAAATCGGCCCGCAGGGGTCTCT	180
Oy	61	AspArgPheSerGlySerIleYsSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg	80
Db	181	GACCAATTCTCTGGGTCTCCAAAGCTTGACACTTCAGCCTCTCGGCTATACATGGGTTCCGT	240

QY	81	SerGUhspGCUuaIaaAPYrTTCyCaAlaAlaArtpspSspSerLeuSerGlyTTPVaI	100
Db	241	TCCAGAGATGAGCGCTGATATTACTGTGCACAGATGAGATTAATTCTTGTCTGGTTGGGTG	300
QY	101	PheGlyGlyGlyThrIlySLeuthrThaIleugly	111
Db	301	TTCCGGCGAGGAGCACGAGCTGACCGTCTTAGGT	333
RESULT 14			
LOCUS	HSU38340	333 bp	mRNA linear PRI 02-OCT-1996
DEFINITION	Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,		
ACCESSION	U38340		
VERSION	U38340.1	GI:1145341	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
REFERENCE	Hominidae; Homo.		
AUTHORS	1 (bases 1 to 333)		
	Schlier,R., Ballint,R.F., McCall,A., Apell,G., Larrick,J.W. and		
	Marks,J.D.		
TITLE	Identification of functional and structural amino-acid residues by		
JOURNAL	parsonious mutagenesis		
PUBMED	Gene 169 (2), 147-155 (1996)		
REFERENCE	8647439		
AUTHORS	2 (bases 1 to 333)		
	Schlier,R., Ballint,R.F., McCall,A., Apell,G., Larrick,J.W. and		
	Marks,J.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-OCT-1995) Robert Schlier, Anesthesia, UC San		
	Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA		
FEATURES	Location/Qualifiers		
source	1..333		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CGPM6"		
	/clone_1id="semisynthetic scFv phage display library"		
	<1..>333		
CDS	/codon_start=1		
	/product="anti-c-erbB-2 immunoglobulin light chain V"		
	/protein_id="AAB09650.1"		
	/db_xref="GI:1145342"		
	/translation="QSVLTQPPSYSAAPGQKVTITSCGSSSNIGKNYVSYYQDLPGTA		
	PKLIAGRYINRPAQVDPDRFSGSKSGTASLAIISGFRSEADADYYCAAMDVSLSGWVFG		
	GTRLTVAIG"		
ORIGIN			
Alignment Scores:			
Pred. No.:	4.47e-52	Length:	333
Score:	562.00	Matches:	107
Percent Similarity:	97.3%	Conservative:	1
Best Local Similarity:	96.4%	Mismatches:	3
Query Match:	95.6%	Indels:	0
DB:	5	Gaps:	0
US-10-0992-640-36 (1-111) x HSU38340 (1-333)			
QY	1	GInSerValLeuThrInpProProSerValSerAlaIaIaProGlyInIlyValThrIle	20
Db	1	CAGTCTGTGTTGAAGCAGCGCGCCTCTAGTGTCTCGGCCCCAGACAGAGGTACCATC	60
QY	21	SeiCySseGjySerSerSerSerAsnIleGlyAsnAsnTyValSerTPYrGInGInIleu	40
Db	61	TCTGCTCTGGAACAGACTCCAAATTCATGTTAAATTAATTCATCTCTGTACACAGACTC	120
QY	41	ProGlyThrAlaPProIySLeuLeuIleTyGlyIhIsthRAsnAAGProAlaGlyValPro	60
Db	121	CCAGAAACAGCCCCAACTCTCATCTATGTCGTGCACCAATGAGCCCGAGGGAGTCTCT	180

QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 DB 181 GACCGATTCTCTGCTCCAGAGCTGAGCACTCCAGCTCCCTGCTATCACTGGGCTCCGG 240
 QY 81 SerGluAspGluAlaAspTyrTyrCySAAlaAlaTrpAspAspSerLeuSerGlyTTPVal 100
 DB 241 TCCGAGGATGAGGCTGATTATTACTGTGCGACGATGGATTATCTTTGTTGGTGGTG 300
 QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
 DB 301 TTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 333

RESULT 15
 HSU38344 333 bp mRNA linear PRI 02-OCT-1996
 LOCUS Human anti-c-erbB-2 immunoglobulin light chain V mRNA, partial cds,
 DEFINITION clone C6PM10.
 ACCESSION U38344
 VERSION U38344.1 GI:1145349
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 333)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.
 TITLE Identification of functional and structural amino-acid residues by
 JOURNAL paratimonous mutagenesis
 PUBLISHED Gene 169 (2), 147-155 (1996)
 REFERENCE 2 (bases 1 to 333)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
 Marks, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
 Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 FEATURES
 source
 1.333
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C6PM10"
 /clone_lib="semisynthetic scFv phage display library"
 <1..>333
 /codon_start=1
 /product="anti-c-erbB-2 immunoglobulin light chain V"
 /protein_id="AAB09654.1"
 /db_xref="GI:1145350"
 /translation="OSVLTQPPSVSAAPQKVTISCGSSSNIGNDYVSWYQQLPGTA
 PKLLIYGHTNRPAVGVDPRFSKSGTSASLAISGRSEADADYYCAPMDASQYGVWFG
 GGTKLTVLG"

CDs
 /product="anti-c-erbB-2 immunoglobulin light chain V"
 /protein_id="AAB09654.1"
 /db_xref="GI:1145350"
 /translation="OSVLTQPPSVSAAPQKVTISCGSSSNIGNDYVSWYQQLPGTA
 PKLLIYGHTNRPAVGVDPRFSKSGTSASLAISGRSEADADYYCAPMDASQYGVWFG
 GGTKLTVLG"

ORIGIN

Alignment Scores:
 Pred. No.: 1.22e-51 Length: 333
 Score: 558.00 Matches: 106
 Percent Similarity: 96.4% Conservative: 1
 Best Local Similarity: 95.5% Mismatches: 4
 Query Match: 94.9% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-36 (1-111) X HSU38344 (1-333)

QY 1 GlnSerValLeuThrGlnProPProSerValSerAlaAlaProGlyGlnIysValThrIle 20
 DB 1 CAGTCTGTGTGACGACGCGCCCTCAGTCTGCGCGCCCGACAGACGAAAGGTCCACCATC 60
 QY 21 SerCySerGlySerSerSerAenIleGlyAsnAsnTyrValSerTTPYrGlnGlnLeu 40
 DB 61 TCTGTCTTGGAAGCAGCTCCAACTTGGGAGATATTATGTATCTGTGTAACGACGAGCTC 120

QY 41 ProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
 DB 121 CCAGGAACAGCCCCCAAACTCCATCTATGATGACACCAATGAGCCCGAGGGGTCCCT 180
 QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 DB 181 GACCGATTCTCTGCTCCAGAGCTGAGCACTCCAGCTCCCTGCGCATCACTGGGTTCCGG 240
 QY 81 SerGluAspGluAlaAspTyrTyrCySAAlaAlaTrpAspAspSerLeuSerGlyTTPVal 100
 DB 241 TCCGAGGATGAGGCTGATTATTACTGTGCGCGCTGGGAGCGCTCCAGTACGGGTGGGTG 300
 QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
 DB 301 TTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 333

Search completed: May 25, 2006, 19:00:43
 Job time : 4227.86 secs

This Page Blank (uspo7c)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:10:39 ; Search time 473.138 Seconds

(without alignments)
2453.577 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588
Sequence: 1 QSVLRQPPVSAAPGQKVTI.....MDDSLSGWVGSGTKLTVLG 111

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abs/ABSSMBE.epool/US10092640/runat_25052006_155711_5825/app.query.fasta_1
-DB=N.Geneseq -QFMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs05h
-USER=US10092640@CGN_1_1_942_@runat_25052006_155711_5825 -MCPD=6 -ICPD=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -GAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_8: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *
15: geneseqn2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	588	100.0	765	AAD32664 Chimeric
2	588	100.0	774	AAT50787 C6 human
3	566	96.3	807	AAD32665 Chimeric

Result ID	Score	Query Match Length	ID	Description
1	588	100.0	765	AAD32664 Chimeric
2	588	100.0	774	AAT50787 C6 human
3	566	96.3	807	AAD32665 Chimeric

```

XX 03-JAN-2002.
PD 25-JUN-2001; 2001WO-US020182.
XX 23-JUN-2000; 2000US-0213653P.
XX (HUST/) HUSTON J S.
PA (WILS/) WILS P.
PA (QUAN/) QUAN Z.
PA (LAUR/) LAURENT O.
PA (MARASCO/) MARASCO W A.
PA (SCHE/) SCHERMAN D.
XX Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
PI WPI; 2002-268789/31.
DR P-PSDB; AAE20407.
XX
XX Gene-delivery compound for targeted gene delivery, comprises single-chain
PT binding polypeptide having effector segment with cysteinyl residue and
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
PT residue.
XX
XX Disclosure; Fig 4; 96pp; English.
XX
XX The invention relates to gene-delivery compound comprising a single-chain
CC binding polypeptide (SCBP) having at least one effector segment having a
CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
CC compound is useful for targeted gene delivery for treating diseases by
CC gene therapy. The present sequence is chimeric SCBP C6.5 sFv DNA
CC comprising human and murine sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 765 BP; 155 A; 217 C; 227 G; 166 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.56e-47 Length: 765
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-092-640-36 (1-111) x AAD32664 (1-765)
QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20
DB 433 CAGTCTGTTTACGCGAGCCGCCCTCAGTGTCTGCGGCCCCAGACAGAGGTCACATC 492
QY 21 SerCysSerGlySerSerSerSerSerAnIleGlyAsnSerTrpValSerTrpTyrGlnGlnLeu 40
DB 493 TCTCTGCTCTGGAAGCAGCTCCCAATGGGAATTAATATGATCCGTGACAGCAGCTC 552
QY 41 ProGlyThrAlaProIysLeuLeuIleTyrGlyIleHisThrAspArgProIleGlyValPro 60
DB 553 CCAAGGAACGCCCCCAACTCCCATCTATGTCACACCAATCGGCCCGAGGGGCTCCCT 612
QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 613 GACCGATTCTCTGGCTCCCAAGTCTGGCACTCACTCCCTGCGCCATCAGTGGTTCCGG 672
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTrpAspSerLeuSerGlyTyrVal 100
DB 673 TCCGAGGATGAGGCTGATTAATTACTGTGACGATCGGATGACAGCTGAGTGGTGGTG 732
QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
DB 733 TTGGGCGAGGAGCAAGCTGACCGTCTAGGT 765

```

```

ID AAT50787 standard; DNA; 774 BP.
XX
XX AAT50787;
AC 23-SEP-1997 (first entry)
XX
XX C6 human sFv antibody C6.5 encoding DNA.
DE C6 human sFv antibody C6.5 encoding DNA.
XX
XX Tumour; immune response; cytotoxin; carcinoma; breast cancer; ss.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..774
FT
FT /*tag= a
FT /product= "Antibody_C6.5"
FT /transl_except= (pos: 181..183, aa: Ser)
FT /transl_except= (pos: 361..363, aa: Gly)
FT /transl_except= (pos: 421..423, aa: Gly)
FT /note= "Without stop codon"
XX
XX WO9700271-A1.
XX
XX 03-JAN-1997.
XX
XX 13-JUN-1996; 96WO-US010287.
XX
XX 14-JUN-1995; 95US-0000238P.
XX 15-JUN-1995; 95US-0000250P.
XX
XX (BEGC ) UNIV CALIFORNIA.
XX
XX Marks JD, Schier R;
PI WPI; 1997-077488/07.
XX P-PSDB; AAW08487.
XX
XX New C6 human antibody binding specifically to c-erbB-2 - useful for
PT treatment and diagnosis of tumours, with reduced risk of generating
PT immune response.
XX
XX Claim 4; Fig 1; 117pp; English.
XX
XX The present sequence encodes a C6 human antibody C6.5, that binds
CC specifically to c-erbB-2. A chimeric molecule that binds specifically to
CC tumour cells carrying c-erbB-2 consists of an effector compound attached
CC to a C6 human antibody, e.g. C6.5. If the effector compound is a
CC cytotoxin the chimeric molecule can be used to inhibit growth of c-erbB-2
CC positive tumours (especially breast and other carcinomas). If the
CC effector compound is a label the chimeric molecule can be used to detect
CC such cells, including in vivo localisation. The antibody can also be used
CC for diagnosis/localisation, in vivo or in vitro, especially by
CC immunoassay. The nucleic acid encoding the antibody, and a nucleic acid
CC encoding a single chain polypeptide with the binding specificity of the
CC antibody and comprising the binding portions of variable regions of light
CC and heavy chains of the antibody, joined by a linker, can be used to
CC produce recombinant proteins by standard methods. Unlike known anti-c-
CC erbB-2 antibodies, C6 antibodies are fully human, so should elicit
CC little, if any, immunogenic response
XX
XX Sequence 774 BP; 156 A; 222 C; 230 G; 166 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.56e-47 Length: 774
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-092-640-36 (1-111) x AAT50787 (1-774)
QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20

```

```

Db      433 CAGTCTGTGTGAACGACCCGCTCAGTGTCTGGGCCCCAGAGACAGAAAGTCCACCATC 492
Qy      21 SerCySerGlySerSerSerAsnIleGlyAsnAsnTyValSerTrpTyrgInIleu 40
Db      493 TCCTGCTCTGGAGAGAGAGCTCCACATTGGGAATATATTATCTCTGGTACCGAGAGCTC 552
Qy      41 ProGlyThrAlaProIysLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
Db      553 CCAGGAACAGAGCCCAAACTCCATCTATGTCACACCAATCGGCGCCGAGGGGATCCCT 612
Qy      61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      613 GACCGATTCTCTGCTCCAGCTCGACCTGACCTCCTGGCCATCAGTGGGTTCCGG 672
Qy      81 SerGluAspGluAlaAspTyTyTyCyAlaAlaATrpaSpsAspSerLeuSerGlyTrpVal 100
Db      673 TCCGAGGATGAGGCTGATTATTACTGTGACAGCATGGGATGACAGCTGAGTTGGGTG 732
Qy      101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
Db      733 TTCGGCGAGAGGACCAAGCTGACCGTCTTAGGT 765

RESULT 3
AAD32665
ID      AAD32665 standard; DNA; 807 BP.
AC      AAD32665;
DT      29-AUG-2003 (revised)
DT      18-JUN-2002 (first entry)
XX      Chimeric SCBP C6ML3-9 sfv' DNA.
DE      Chimeric SCBP C6ML3-9 sfv' DNA.
XX      Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
XX      nucleic acid-binding moiety; NAM; lipid-associating moiety; LAM;
XX      gene therapy; targeted gene delivery; human; murine; chimeric; ds.
OS      Homo sapiens.
OS      Mus sp.
OS      Chimeric.
XX      Key      Location/Qualifiers
FH      CDS      1..807
FT      /*tag= a
FT      /product= "Chimeric SCBP C6ML3-9 sfv' protein"
FT      /note= "CDS does not include start and stop codon"
XX      /partial
XX      MO200200914-A2.
XX      ID      AAD32666 standard; DNA; 846 BP.
XX      AC      AAD32666;
XX      DT      29-AUG-2003 (revised)
XX      DT      18-JUN-2002 (first entry)
XX      DE      Chimeric SCBP C6ML-3-9sfv'-L1-KDEL DNA.
XX      KW      Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
XX      nucleic acid-binding moiety; NAM; lipid-associating moiety; LAM;
XX      gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX      OS      Homo sapiens.
XX      OS      Mus sp.
XX      OS      Chimeric.
XX      Key      Location/Qualifiers
FH      CDS      1..846
FT      /*tag= a
FT      /product= "Chimeric SCBP C6ML-3-9sfv'-L1-KDEL protein"
FT      /note= "CDS does not include start and stop codon"
XX      /partial
XX      WPI; 2002-268789/31.
XX      Gene-delivery compound for targeted gene delivery, comprises single-chain
XX      binding polypeptide having effector segment with cysteinyl residue and
XX      nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
XX      residue.

```

```

PS      Disclosure; Fig 6; 96pp; English.
XX      CC      The invention relates to gene-delivery compound comprising a single-chain
XX      CC      binding polypeptide (SCBP) having at least one effector segment having a
XX      CC      cysteinyl residue, and a nucleic acid-binding moiety (NAM) or a lipid-
XX      CC      associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
XX      CC      compound is useful for targeted gene delivery for treating diseases by
XX      CC      gene therapy. The present sequence is chimeric SCBP C6ML3-9 sfv' DNA
XX      CC      comprising human and murine sequences. (Updated on 29-AUG-2003 to
XX      CC      standardise OS field)
SQ      Sequence 807 BP; 160 A; 240 C; 237 G; 170 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.:      6.11e-45      Length:      807
Score:          566.00      Matches:      107
Percent Similarity: 98.2%      Conservative: 2
Best Local Similarity: 96.4%      Mismatches: 2
Query Match:    96.3%      Indels:      0
DB:             6      Gaps:        0

US-10-092-640-36 (1-111) x AAD32665 (1-807)
Qy      1 GluSerValIleuThrGlnProPseSerValSerAlaAlaProGlyGlnIysValThrIle 20
Db      433 CAGTCTGTGTGAACGACCCGCTCAGTGTCTGGGCCCCAGAGACAGAAAGTCCACCATC 492
Qy      21 SerCySerGlySerSerSerAsnIleGlyAsnAsnTyValSerTrpTyrgInIleu 40
Db      493 TCCTGCTCTGGAGAGAGAGCTCCACATTGGGAATATATTATCTCTGGTACCGAGAGCTC 552
Qy      41 ProGlyThrAlaProIysLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
Db      553 CCAGGAACAGAGCCCAAACTCCATCTATGTCACACCAATCGGCGCCGAGGGGATCCCT 612
Qy      61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      613 GACCGATTCTCTGCTCCAGCTCGACCTGACCTCCTGGCCATCAGTGGGTTCCGG 672
Qy      81 SerGluAspGluAlaAspTyTyTyCyAlaAlaATrpaSpsAspSerLeuSerGlyTrpVal 100
Db      673 TCCGAGGATGAGGCTGATTATTACTGTGCTCTGGGATGACAGCTGAGTTGGGTG 732
Qy      101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
Db      733 TTCGGCGAGAGGACCAAGCTGACCGTCTTAGGT 765

RESULT 4
AAD32666
ID      AAD32666 standard; DNA; 846 BP.
AC      AAD32666;
XX      DT      29-AUG-2003 (revised)
XX      DT      18-JUN-2002 (first entry)
XX      DE      Chimeric SCBP C6ML-3-9sfv'-L1-KDEL DNA.
XX      KW      Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
XX      nucleic acid-binding moiety; NAM; lipid-associating moiety; LAM;
XX      gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX      OS      Homo sapiens.
XX      OS      Mus sp.
XX      OS      Chimeric.
XX      Key      Location/Qualifiers
FH      CDS      1..846
FT      /*tag= a
FT      /product= "Chimeric SCBP C6ML-3-9sfv'-L1-KDEL protein"
FT      /note= "CDS does not include start and stop codon"
XX      /partial

```

PN WO200200914-A2.
 XX 03-JAN-2002.
 XX 25-JUN-2001; 2001WO-US020182.
 XX 23-JUN-2000; 2000US-0213653P.
 XX (HUST/) HUSTON J S.
 PA (WILS/) WILS P.
 PA (QUAN/) QUAN Z.
 PA (LAUR/) LAURENT O.
 PA (MARA/) MARASCO W A.
 PA (SCHE/) SCHERMAN D.
 XX
 PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
 DR WPI; 2002-268789/31.
 DR P-PSDB; AAE20409.
 XX
 PT Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
 PT residue.
 XX
 XX Example 2; Fig 8; 96pp; English.
 XX
 CC The invention relates to gene-delivery compound comprising a single-chain
 CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFv'-L2-KDEL
 CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 846 BP; 171 A; 250 C; 246 G; 179 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,45e-45 Length: 846
 Score: 566.00 Matches: 107
 Percent Similarity: 98.2% Conservative: 2
 Best Local Similarity: 96.4% Mismatches: 2
 Query Match: 96.3% Indels: 0
 DB: 6 Gaps: 0

US-10-092-640-36 (1-111) x AAD32666 (1-846)

QY 1 GlnSerValIleuThrGlnProProSerValSerAlaAlaProGlyGlnIleValThrIle 20
 DB 433 CAGTCTGTGTGACGAGCGCCGCTCAGTGTCTGCGGCCCCAGAGACAGAGGTCAACCATC 492
 QY 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTrpValSerTrpTyrGlnGlnIleu 40
 DB 493 TCCTGCTGTGGAAGCAGCTCCAAACATGGGAATTAATTATGATCCGGAACAGCAGCTC 552
 QY 41 ProGlyThAlaProIleuIleuIleTyrGlyHisThAsnArgProIleGlyValPro 60
 DB 553 CAGGAACAGCCCCCAACTCTCATCTATGATACACCAATCGGCCCCAGAGGGGCTCT 612
 QY 61 AspArgPheSerGlySerIleSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
 DB 613 GACCGATTCTGGGCTCCCAAGTCTGSCACTCAGCTCTCCCTGCCATCATGTTGCGG 672
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTyrAspSerIleuSerGlyTyrVal 100
 DB 673 TCCGAGGATGAGGCTGATTAATTACTGTGCTCTCGGACTACACCTCTCGGGCTGGGTG 732
 QY 101 PheGlyGlyGlyThrIleuThrValIleuGly 111
 DB 733 TTGCGGAGGAGAACCAAGCTGACGCTCTAGGT 765

RESULT 5

AAD32667
 ID AAD32667 standard; DNA; 861 BP.
 XX
 AC AAD32667;
 XX
 DT 29-AUG-2003 (revised)
 DT 18-JUN-2002 (first entry)
 XX
 DE Chimeric SCBP C6ML-3-9sFv'-L2-KDEL DNA.
 XX
 KW Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
 KW nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
 KW gene therapy; targeted gene delivery; human; murine; chimeric; ds.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..861
 FT /*tag= a
 FT /product= "Chimeric SCBP C6ML-3-9sFv'-L2-KDEL protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX
 PN WO200200914-A2.
 XX
 XX 03-JAN-2002.
 XX 25-JUN-2001; 2001WO-US020182.
 XX 23-JUN-2000; 2000US-0213653P.
 XX (HUST/) HUSTON J S.
 PA (WILS/) WILS P.
 PA (QUAN/) QUAN Z.
 PA (LAUR/) LAURENT O.
 PA (MARA/) MARASCO W A.
 PA (SCHE/) SCHERMAN D.
 XX
 PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
 DR WPI; 2002-268789/31.
 DR P-PSDB; AAE20410.
 XX
 PT Gene-delivery compound for targeted gene delivery, comprises single-chain
 PT binding polypeptide having effector segment with cysteinyl residue and
 PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
 PT residue.
 XX
 XX Example 2; Fig 10; 96pp; English.

PS The invention relates to gene-delivery compound comprising a single-chain

CC binding polypeptide (SCBP) having at least one effector segment having a
 CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
 CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
 CC compound is useful for targeted gene delivery for treating diseases by
 CC gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFv'-L2-KDEL
 CC DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 861 BP; 173 A; 255 C; 250 G; 183 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.58e-45 Length: 861
 Score: 566.00 Matches: 107
 Percent Similarity: 98.2% Conservative: 2
 Best Local Similarity: 96.4% Mismatches: 2
 Query Match: 96.3% Indels: 0
 DB: 6 Gaps: 0

US-10-092-640-36 (1-111) x AAD32667 (1-861)

```

Qy      1 GlnSerValIeuThrGlnProSerValSerAlaIaProGlyGlnIlyValThrIle 20
Db      433 CAGTCTGTGTGACGACGCCCTCAGTGTCTGGGCCCCAGGACAGAAAGTACCATC 492
Qy      21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyValSerTPYrGlnGlnIleu 40
Db      493 TCCGTGCTCTGGAAGACACTCCAACTGGGAATATATGATCTCTGTACACGACACTC 552
Qy      41 ProGlyThrAlaProIlyLeuIleIlyGlyVhiThrAsnArgProAlaGlyValPro 60
Db      553 CCAGGAACACGCCCCCAAACTCTCATCTATGATCACCACCAATCGGCCGAGGGGTCCCT 612
Qy      61 AspArgPheSerGlySerIlySerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
Db      613 GACCGATTCTTGCTGCTCAAGTCTGSCACCTCAGCTCCCTGGCCATCAGTGGGTCCGG 672
Qy      81 SerGluAspGluIaAspTYrTYrCysAlaIaIaTrpAspAspSerIleuSerGlyTyrPval 100
Db      673 TCCGAGGATGAGGTGATTTATTTACTGTGCTCTCGGACCTACACCCCTCTCGGGCTGGGTG 732
Qy      101 PheGlyGlyGlyThrIlyLeuThrValIleuGly 111
Db      733 TTCGGCGAGAGAACCAAGCTGACCGTCTTAGT 765

RESULT 6
AAD32669
ID      AAD32669 standard; DNA; 873 BP.
XX
AC      AAD32669;
XX
DT      29-AUG-2003 (revised)
DT      18-JUN-2002 (first entry)
XX
DE      Chimeric SCBP C6ML-3-9sFv'-I2-nls DNA.
KM      Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KM      nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KM      gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX
OS      Homo sapiens.
OS      Mus sp.
OS      Chimeric.
XX
FH      Key
FH      CDS
FT      1. .873
FT      /tag= a
FT      /product= "Chimeric SCBP C6ML-3-9sFv'-I2-nls protein"
FT      /note= "CDS does not include start and stop codon"
FT      /partial
XX
XX      WO200200914-A2.
XX
XX      03-JAN-2002.
XX
XX      25-JUN-2001; 2001WO-US020182.
XX
XX      23-JUN-2000; 2000US-0213653P.
XX
XX      (HUST/) HUSTON J S.
XX      (WILS/) WILS P.
XX      (QUAN/) QUAN Z.
XX      (LAUR/) LAURENT O.
XX      (MARA/) MARASCO W A.
XX      (SCHE/) SCHERMAN D.
XX
XX      Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX      MPI; 2002-268789/31.
XX      P-PSDB; AAE20412.
XX
XX      Gene-delivery compound for targeted gene delivery, comprises single-chain
XX      binding polypeptide having effector segment with cysteinyl residue and
XX      nucleic acid-binding/lipid-associating moiety coupled to polypeptide by

```

```

PT      residue.
XX
XX      Example 2, Fig 14; 96pp; English.
PS
XX
CC      The invention relates to gene-delivery compound comprising a single-chain
CC      binding polypeptide (SCBP) having at least one effector segment having a
CC      cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
CC      associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
CC      compound is useful for targeted gene delivery for treating diseases by
CC      gene therapy. The present sequence is chimeric SCBP C6ML-3-9sFv'-I2-nls
CC      DNA comprising human and murine sequences. (Updated on 29-AUG-2003 to
CC      standardise OS field)
XX
SQ      Sequence 873 BP; 177 A; 260 C; 252 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      6,69e-45      Length:      873
Score:          566.00      Matches:      107
Percent Similarity: 98.2%      Conservative: 2
Best Local Similarity: 96.4%      Mismatches: 2
Query Match:     96.3%      Indels:      0
DB:              Gaps:      0

US-10-092-640-36 (1-111) x AAD32669 (1-873)

Qy      1 GlnSerValIeuThrGlnProSerValSerAlaIaProGlyGlnIlyValThrIle 20
Db      433 CAGTCTGTGTGACGACGCCCTCAGTGTCTGGGCCCCAGGACAGAAAGTACCATC 492
Qy      21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyValSerTPYrGlnGlnIleu 40
Db      493 TCCGTGCTCTGGAAGACACTCCAACTGGGAATATATGATCTCTGTACACGACACTC 552
Qy      41 ProGlyThrAlaProIlyLeuIleIlyGlyVhiThrAsnArgProAlaGlyValPro 60
Db      553 CCAGGAACACGCCCCCAAACTCTCATCTATGATCACCACCAATCGGCCGAGGGGTCCCT 612
Qy      61 AspArgPheSerGlySerIlySerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
Db      613 GACCGATTCTTGCTGCTCAAGTCTGSCACCTCAGCTCCCTGGCCATCAGTGGGTTCGG 672
Qy      81 SerGluAspGluIaAspTYrTYrCysAlaIaIaTrpAspAspSerIleuSerGlyTyrPval 100
Db      673 TCCGAGGATGAGGTGATTTATTTACTGTGCTCTCGGACCTACACCCCTCTCGGGCTGGGTG 732
Qy      101 PheGlyGlyGlyThrIlyLeuThrValIleuGly 111
Db      733 TTCGGCGAGAGAACCAAGCTGACCGTCTTAGT 765

RESULT 7
AAD32668
ID      AAD32668 standard; DNA; 888 BP.
XX
AC      AAD32668;
XX
DT      29-AUG-2003 (revised)
DT      18-JUN-2002 (first entry)
XX
DE      Chimeric SCBP C6ML-3-9sFv'-I2-H14 DNA.
KM      Gene-delivery compound; single-chain binding polypeptide; SCBP; gene;
KM      nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;
KM      gene therapy; targeted gene delivery; human; murine; chimeric; ds.
XX
OS      Homo sapiens.
OS      Mus sp.
OS      Chimeric.
XX
FH      Key
FH      CDS
FT      1. .888
FT      /tag= a
FT      /product= "Chimeric SCBP C6ML-3-9sFv'-I2-H14 protein"
FT      /note= "CDS does not include start and stop codon"
FT

```


PT at least one oxidized fragment of apolipoprotein B in the manufacture of
 PT a pharmaceutical composition for treating atherosclerosis.

PS Claim 6; SEQ ID NO 6; 84pp; English.

XX The present invention describes the use of at least one isolated human
 CC antibody or antibody fragment directed towards at least one oxidised
 CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
 CC composition for treatment of atherosclerosis by means of passive
 CC immunisation. Also described: (1) preparing the isolated antibody; (2)
 CC amplifying the isolated human antibody; (3) passive immunisation of
 CC mammals; and (4) a pharmaceutical composition comprising the isolated
 CC human antibody directed towards at least one oxidised fragment of
 CC apolipoprotein B for treatment of atherosclerosis by means of passive
 CC immunisation, where the antibody is present in combination with a
 CC pharmaceutical excipient. The human antibody has antiarteriosclerotic
 CC activity. The isolated human antibody or antibody fragment directed
 CC towards at least one oxidised fragment of apolipoprotein B is useful in
 CC the manufacture of a pharmaceutical composition for treatment of
 CC atherosclerosis by means of passive immunisation. The present sequence
 CC represents a variable light region (VL) of an anti-apolipoprotein B
 CC antibody from the present invention.

SQ Sequence 333 BP; 66 A; 99 C; 93 G; 75 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,27e-43 Length: 333
 Score: 545.00 Matches: 102
 Percent Similarity: 95.5% Conservative: 4
 Best Local Similarity: 91.9% Mismatches: 5
 Query Match: 92.7% Indels: 0
 DB: 12 Gaps: 0

US-10-092-640-36 (1-111) x ADM98139 (1-333)

QY 1 GlnSerValIleuThGlnProProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
 DB 1 CAGTCTGTGCTGACTGACGACCCCTCAGGGTCTGGAGCCCGGGGAGGGGTACATC 60
 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
 DB 61 TCTTGTCTGGAAGCGCTCCCAATATCGAAGATTAATATATCCGATACGCGACTC 120
 QY 41 ProGlyThrAlaProIlySerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60
 DB 121 CAGGAGAGGCCCCCAACTCTCTCATCTATGTAATCAATCGGCCCTCAGGGTCCCT 180
 QY 61 AspArgPheSerGlySerIlySerSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
 DB 181 GACCATTTCTTGCTCCAGCTCCCAAGTCTGACACTCGCTCCCTGGCCATCATGTCGCTCCG 240
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTPAspAspSerIleuSerGlyTyrPVal 100
 DB 241 TCCGAGATGAGAGCTGATTAATTAATCTGACGATGGATGACAGCTCGATGTTGGGTG 300
 QY 101 PheGlyGlyGlyThrIlySerIleuThrValIleuGly 111
 DB 301 TTGGCGGAGAGAACCAAGCTGACGCTCCTAGGT 333

RESULT 11

ADM98163
 ID ADM98163 standard; DNA; 333 BP.

XX ADM98163;

XX 01-JUL-2004 (first entry)-

DE Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:30.
 XX human antibody; antibody, apolipoprotein B; atherosclerosis;
 XX passive immunisation; antiarteriosclerotic; variable light region; VL;
 KW anti-apolipoprotein B antibody; gene; ds.
 XX

OS Homo sapiens.
 OS Synthetic.

PN WO2004030607-A2.

XX 15-APR-2004.

PF 06-OCT-2003; 2003WO-SE001547.

PR 04-OCT-2002; 2002SE-00002959.

PR 27-AUG-2003; 2003SE-00002312.

PR 22-SEP-2003; 2003WO-SE001469.

XX (FORS-) FORSKARPATENT I SYD AB.

PI Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
 DR WPI; 2004-316320/29.

PT Use of an isolated human antibody or antibody fragment directed towards
 PT at least one oxidized fragment of apolipoprotein B in the manufacture of
 PT a pharmaceutical composition for treating atherosclerosis.

PS Claim 6; SEQ ID NO 30; 84pp; English.

XX The present invention describes the use of at least one isolated human
 CC antibody or antibody fragment directed towards at least one oxidised
 CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
 CC composition for treatment of atherosclerosis by means of passive
 CC immunisation. Also described: (1) preparing the isolated antibody; (2)
 CC amplifying the isolated human antibody; (3) passive immunisation of
 CC mammals; and (4) a pharmaceutical composition comprising the isolated
 CC human antibody directed towards at least one oxidised fragment of
 CC apolipoprotein B for treatment of atherosclerosis by means of passive
 CC immunisation, where the antibody is present in combination with a
 CC pharmaceutical excipient. The human antibody has antiarteriosclerotic
 CC activity. The isolated human antibody or antibody fragment directed
 CC towards at least one oxidised fragment of apolipoprotein B is useful in
 CC the manufacture of a pharmaceutical composition for treatment of
 CC atherosclerosis by means of passive immunisation. The present sequence
 CC represents a variable light region (VL) of an anti-apolipoprotein B
 CC antibody from the present invention.

SQ Sequence 333 BP; 65 A; 104 C; 93 G; 71 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.65e-42 Length: 333
 Score: 536.00 Matches: 100
 Percent Similarity: 94.6% Conservative: 5
 Best Local Similarity: 90.1% Mismatches: 6
 Query Match: 91.2% Indels: 0
 DB: 12 Gaps: 0

US-10-092-640-36 (1-111) x ADM98163 (1-333)

QY 1 GlnSerValIleuThGlnProProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
 DB 1 CAGTCTGTGCTGACTGACGACCCCTCAGGGTCTGGAGCCCGGGGAGGGGTACATC 60
 QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
 DB 61 TCTGCTCTGGAAGACCTCCCAATCTCTCATCTATGTAATCAATCGGCCCTCAGGGTCCCT 120
 QY 41 ProGlyThrAlaProIlySerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60
 DB 121 CAGGAGAGGCCCCCAACTCTCTCATCTATGTAATCAATCGGCCCTCAGGGTCCCT 180
 QY 61 AspArgPheSerGlySerIlySerSerGlyThrSerAlaSerIleuAlaIleSerGlyPheArg 80
 DB 181 GACCATTTCTTGCTCCAGCTCCCAAGTCTGACACTCGCTCCCTGGCCATCATGTCGCTCCG 240
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTPAspAspSerIleuSerGlyTyrPVal 100

Db 241 TCCGAGATGAGGCTGATTACTGTCGACGATGGGATGCCAGCTCAGTGGTGGTG 300
 QY 101 PheGlyGlyGlyThrylsLeuThrValLeuGly 111
 Db 301 TTCGGCGAGAACCAAGCTGACGCTCTAGGT 333
 RESULT 12
 ID ADN00515 standard; DNA; 336 BP.
 AC ADN00515;
 DT 01-JUL-2004 (first entry)
 DE Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:2.
 XX
 XX human antibody; antibody; apolipoprotein B; atherosclerosis;
 KM passive immunisation; antiarteriosclerotic;
 KM anti-apolipoprotein B antibody; variable light region; VL; gene; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO2004030698-A1.
 XX
 PD 15-APR-2004.
 PF 22-SEP-2003; 2003WO-SE001469.
 PR 04-OCT-2002; 2002SE-00002959.
 PR 27-AUG-2003; 2003SE-00002312.
 XX
 PA (FORS-) FORSKARPATENT I SYD AB.
 PI Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
 XX
 DR WPI; 2004-316343/29.
 PT Use of a recombinant human antibody or antibody fragment directed towards
 PT at least one oxidized fragment of apolipoprotein B for the manufacture of
 PT a pharmaceutical composition for treating atherosclerosis.
 XX
 PS Claim 5; SEQ ID NO 2; 59pp; English.
 CC The present invention describes the use of at least one recombinant human
 CC antibody or antibody fragment directed towards at least one oxidised
 CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
 CC composition for treatment of atherosclerosis by means of passive
 CC immunisation. Also described: (1) preparing the isolated antibody; (2)
 CC amplification of isolated human antibody; (3) passive immunisation of
 CC mammals; and (4) a pharmaceutical composition comprising the recombinant
 CC human antibody directed towards at least one oxidised fragment of
 CC apolipoprotein B for treatment of atherosclerosis by means of passive
 CC immunisation. The human antibody has antiarteriosclerotic activity. The
 CC isolated human antibody or antibody fragment directed towards at least
 CC one oxidised fragment of apolipoprotein B is useful in the manufacture of
 CC a pharmaceutical composition for treatment of atherosclerosis by means of
 CC passive immunisation. The present sequence represents a human anti-
 CC apolipoprotein B antibody variable light region (VL) from the present
 CC invention.
 XX
 SQ Sequence 336 BP; 69 A; 101 C; 93 G; 73 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2, 89e-42 Length: 336
 Score: 533.50 Matches: 101
 Percent Similarity: 93.8% Conservative: 4
 Best Local Similarity: 90.2% Mismatches: 6
 Query Match: 90.7% Indels: 1
 DB: 12 Gaps: 1

US-10-092-640-36 (1-111) x ADN00515 (1-336)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
 Db 1 CAGTCTGTGTCGTCAGCCACCTCAGCCTCGGAGACCCCGGAGAGGTCACCATC 60
 QY 21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeu 40
 Db 61 TCCTGCTCTGGAAGACAGGTCCAACTGGGAATTAATTATGTAATCCGTATCAGACGCTC 120
 QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
 Db 121 CCAGAAACGGCCCCCAACTCCATCTATGTATGAACAACATCGCCCTCAGGGGTCCT 180
 QY 61 AspArgPheSerGlySerGlySerGlyTyrThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 181 GACCGATTCCTGCTGCTCCAGCTGCGACCTCAGCCTCCCTGGCCATCAGTGGCTCCGG 240
 QY 81 SerGluAspGluValAspTyrTyrCysAlaAlaTyrAspAspSerLeuSerGly---Tyr 99
 Db 241 TCCGAGATGAGGCTGATTACTGTGTCAGCATGGGATGACAGCTGAATGTCATTGG 300
 QY 100 ValPheGlyGlyGlyThrylsLeuThrValLeuGly 111
 Db 301 GTGTCGCGAGAACCAAGCTGACGCTCTAGGT 336
 RESULT 13
 ID ADM98135 standard; DNA; 336 BP.
 AC ADM98135;
 DT 01-JUL-2004 (first entry)
 DE Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:2.
 XX
 XX human antibody; antibody; apolipoprotein B; atherosclerosis;
 KM passive immunisation; antiarteriosclerotic; variable light region; VL;
 KM anti-apolipoprotein B antibody; gene; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO2004030607-A2.
 XX
 PD 15-APR-2004.
 PF 06-OCT-2003; 2003WO-SE001547.
 PR 04-OCT-2002; 2002SE-00002959.
 PR 27-AUG-2003; 2003SE-00002312.
 PR 22-SEP-2003; 2003WO-SE001469.
 XX
 PA (FORS-) FORSKARPATENT I SYD AB.
 PI Nilsson J, Carlsson R, Bengtsson J, Strandberg L;
 XX
 DR WPI; 2004-316320/29.
 PT Use of an isolated human antibody or antibody fragment directed towards
 PT at least one oxidized fragment of apolipoprotein B in the manufacture of
 PT a pharmaceutical composition for treating atherosclerosis.
 XX
 PS Claim 6; SEQ ID NO 2; 84pp; English.
 CC The present invention describes the use of at least one isolated human
 CC antibody or antibody fragment directed towards at least one oxidised
 CC fragment of apolipoprotein B in the manufacture of a pharmaceutical
 CC composition for treatment of atherosclerosis by means of passive
 CC immunisation. Also described: (1) preparing the isolated antibody; (2)
 CC amplifying the isolated human antibody; (3) passive immunisation of
 CC mammals; and (4) a pharmaceutical composition comprising the isolated
 CC human antibody directed towards at least one oxidised fragment of
 CC apolipoprotein B for treatment of atherosclerosis by means of passive
 CC immunisation, where the antibody is present in combination with a

pharmaceutical excipient. The human antibody has antiarteriosclerotic activity. The isolated human antibody or antibody fragment directed towards at least one oxidised fragment of apolipoprotein B is useful in the manufacture of a pharmaceutical composition for treatment of atherosclerosis by means of passive immunisation. The present sequence represents a variable light region (VL) of an anti-apolipoprotein B antibody from the present invention.

Sequence 336 BP; 69 A; 101 C; 93 G; 73 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.89e+2	Length:	336
Score:	533.50	Matches:	100
Percent Similarity:	93.8%	Conservative:	4
Best Local Similarity:	90.2%	Mismatches:	6
Query Match:	90.7%	Indels:	1
DB:	12	Gaps:	1

US-10-092-640-36 (1-111) X ADM98135 (1-336)

QY	1	HisSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnGlySerValThrIle	20
Db	1	CAGTCTGTGCTACTGACCACTCTAGCGCTCTGGACCCCGGGACAGAGGTCCACCATC	60
QY	21	SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeu	40
Db	61	TCCTGCTCTGGAAAGCAGGTCCAAACATTGGGAATTAATTATGATCCTGGATTACGACGCTC	120
QY	41	ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro	60
Db	121	CCAGGAACGGCCCCCAAACTCCTCAGCTATGGTAACAAACATGGGGCTTCAGAGGGCTCCT	180
QY	61	AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg	80
Db	181	GACGATTTCTCGGCTCCCAAGTCTGGCACCCTCCTCCTGGCCATCAATGGGGCTCCGG	240
QY	81	SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTyrAspAspSerLeuSerGly---Tyr	99
Db	241	TCCGAGGATGAGCGTGAATTATTAATCTGTGACGATGGAGATGACAGCCTGAGTGCATTTGG	300

```

Qy      100 ValpheglyglyglyThrylsleuThrValleucgly 111
        |||||
Db      301 GTGTTGGGGGAGGACCAAGCTACGCTCTAGT 336

```

RESULT 14

ID	ADM98167	standard; DNA; 333 BP.
----	----------	------------------------

AC ADM98167;

DT 01-JUL-2004 (first entry)

DE	Anti-apolipoprotein B antibody variable light region DNA SEQ ID NO:34
XX	human antibody; antibody; apolipoprotein B; atherosclerosis;
KM	passive immunisation; antiarteriosclerotic; variable light region; VL
KW	anti-apolipoprotein B antibody; gene; ds.

OS Homo sapiens.
OS Synthetic.

Synthetic.

PN WO2004030607-A2.

PD 15-APR-2004.

PF 06-OCT-2003; 2003WO-SE001547

PR 04-OCT-2002; 2002SE-00002959

PR 22-SEP-2003; 2003WO-SE001469

PA (FORS-) FORSKARPATENT I SYD A

11

PI Nilsson J, Carlsson R, Bengtsson J, Strandberg L,
XX
DR WPI; 2004-316320/29.

PT Use of an isolated human antibody or antibody fragment directed towards
PT at least one oxidized fragment of apolipoprotein B in the manufacture of
PT a pharmaceutical composition for treating atherosclerosis.

PS Claim 6; SEQ ID NO 34; 84bp; English.

The present invention describes the use of at least one isolated human antibody or antibody fragment directed towards at least one oxidised fragment of apolipoprotein B in the manufacture of a pharmaceutical composition for treatment of atherosclerosis by means of passive immunisation. Also described: (1) preparing the isolated antibody; (2) amplifying the isolated human antibody; (3) passive immunisation of mammals; and (4) a pharmaceutical composition comprising the isolated human antibody directed towards at least one oxidised fragment of apolipoprotein B for treatment of atherosclerosis by means of passive immunisation, where the antibody is present in combination with a pharmaceutical excipient. The human antibody has antiarteriosclerotic activity. The isolated human antibody or antibody fragment directed towards at least one oxidised fragment of apolipoprotein B is useful in the manufacture of a pharmaceutical composition for treatment of atherosclerosis by means of passive immunisation. The present sequence represents a variable light region (VL) of an anti-apolipoprotein B antibody from the present invention.

Sequence 333 BP; 68 A; 102 C; 92 G; 71 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.96e-42	Length:	333
Score:	531.00	Matches:	99
Percent Similarity:	93.7%	Conservative:	5
Best Local Similarity:	89.2%	Mismatches:	7
Query Match:	90.3%	Indels:	0
DB:	12	Gaps:	0

US-10-092-640-36 (1-111) x ADM98167 (1-333)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaIaProGlyGlnLysValThrIle 20
|||||
1 CAGTCTGTTCTGACTACGCCACCTTCAGCGCTTGGAACCCCGGGCAGAGGGGTACCATC 60
Db

ov 21 SerCvssErgIvserSerAsnIleGIvAsnAsnTrvAlSerTrpTrvGInGInLeu 40

Db 61 TCCTGTTCTGGAAGCAGCTCCACATCGGAATAATGGTAACTGGATCAGCAGCTC 120

QY 41 ProGlyThraIaProLysLeuLeuIleTyrgIyHisThraSnaRqProIaGlyValPro 60

Db 121 CCAGGACGGCCCCAACTCCTCATCTATGGTAACAACAATCGCCCTCAGGGTCCCT 180

QY 61 ASDAQPHESERG1YSERLVSSERG1YTHRSERAIASERLEUALAIIESERG1VPHEARQ 80

Db 181 GACCGATTCTTGCTCCAGTCTGGACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240

ov 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGluTrpVal 100

db 241 TCCGAGATGAGGCTGATTATTACTCTGCAGCATGGATGACAGCTTGCCTGGTGGCTG 300

[illegible][illegible]

ADN00521

FDNY 021 OCCIDENTAL, DNY, 000 DE
XX XX

AC ADN00521;
XX

XX
D1 01-005-2004 (11151 ENCLY)

DE Anti-apolipoprotein B antibody variable light region DNA seq ID NO:8.

This Page Blank (uspio)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM proteoin - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:28:39 ; Search time 3650.05 Seconds

(without alignments)
2550.806 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588

Sequence: 1 QSVLRQPSVSAAPGOKVTI.....WDSLSGWVFGGKTUUG 111

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWB.spool/US10092640/runat.25052006.155716.5880/app.query.fasta_1
-DB=EST -QFMT=fastap -SUFPIX=fst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs05h
-USER=US10092640.@CEN.1.1.7986.@runat.25052006.155716.5880 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPO=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	529	90.0	559	9 DA975812	DA975812 DA975812
2	527	89.6	902	3 BQ883560	BQ883560 AGENCOURT
3	519	88.3	490	5 CD692216	CD692216 EST8739 h
4	516.5	87.8	548	9 DA992977	DA992977 DA992977

SUMMARIES

5	516	87.8	494	4	BX283265	BX283265
6	516	87.8	512	2	BM314111	BM314111 in07c03.y
7	516	87.8	656	2	BG755949	BG755949 602716426
8	515.5	87.7	552	9	DA978161	DA978161 DA978161
9	512	87.1	873	2	BG686011	BG686011 602638561
10	511	86.9	780	2	BG535669	BG535669 602563379
11	509	86.6	566	9	DA971136	DA971136 DA971136
12	509	86.6	578	9	DA920210	DA920210 DA920210
13	509	86.6	620	9	DN998001	DN998001 TC103037
14	509	86.6	680	2	BG745508	BG745508 602724089
15	508	86.4	498	7	AM405612	AM405612 UI-HF-BLO
16	507	86.2	574	5	CD689899	CD689899 EST6422 h
17	507	86.2	985	2	BG758331	BG758331 602712522
18	505	85.9	578	5	CD709774	CD709774 EST26301
19	504.5	85.8	620	5	CD696969	CD696969 EST13492
20	503	85.5	561	7	AM406077	AM406077 UI-HF-BLO
21	502	85.4	1029	2	BG760087	BG760087 602733341
22	500	85.0	823	2	BG686957	BG686957 602650951
23	499	84.9	526	9	DA915919	DA915919 DA915919
24	499	84.9	906	2	BF975920	BF975920 602246119
25	498	84.7	419	7	AM631244	AM631244 hn73102.y
26	498	84.7	600	5	CD704266	CD704266 EST20793
27	497	84.5	470	5	CD698832	CD698832 EST15355
28	497	84.5	560	9	DA922062	DA922062 DA922062
29	497	84.5	783	2	BM007830	BM007830 603617507
30	497	84.5	817	2	BG542829	BG542829 602571593
31	496.5	84.4	387	2	BG979831	BG979831 CM4-CN009
32	496	84.4	568	2	BG541474	BG541474 602570918
33	495.5	84.3	567	9	DA929121	DA929121 DA929121
34	494	84.0	730	5	CD709117	CD709117 EST25644
35	493.5	83.9	926	3	BQ706329	BQ706329 AGENCOURT
36	493	83.8	403	7	BE164159	BE164159 QV2-HT046
37	493	83.8	540	3	BP423996	BP423996 BP423996
38	493	83.8	570	9	DA987299	DA987299 DA987299
39	493	83.8	894	3	BQ708570	BQ708570 AGENCOURT
40	492	83.7	400	7	AM406213	AM406213 UI-HF-BLO
41	492	83.7	441	7	AM404093	AM404093 UI-HF-BLO
42	492	83.7	864	2	BG758242	BG758242 602712422
43	492	83.7	936	3	BQ709123	BQ709123 AGENCOURT
44	491	83.5	556	9	DA980170	DA980170 DA980170
45	490.5	83.4	797	4	CB957461	CB957461 AGENCOURT

ALIGNMENTS

RESULT 1	DA975812	559 bp	mRNA	linear	EST 13-nov-2005
LOCUS	DA975812				
DEFINITION	DA975812 SYN0V2 Homo sapiens cDNA clone SYN0V2006376 5', mRNA				
ACCESSION	DA975812				
VERSION	DA975812.1				
KEYWORDS	GI:82348404				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
	1 (bases 1 to 559)				
REFERENCE	Kimura, K., Makamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,				
AUTHORS	Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,				
	Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, K., Kushida, N.,				
	Yoneyama, T., Otsuka, R., Kanada, K., Yokoi, T., Kondo, H., Wagatsuna, M.,				
	Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,				
	Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.				
	Diversification of Transcriptional Modulation: Large-scale				
	Identification and Characterization of Putative Alternative				
	Promoters of Human Genes				
	Genome Res. 16 (1), 55-65 (2006)				
JOURNAL	16344560				
PUBMED	Contact: Takao Isogai				
COMMENT	FLJ Project (HRI Team)				
	Helix Research Institute				

REFERENCE
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
1 (bases 1 to 490)
Lyu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE
Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL
Unpublished (2003)
COMMENT
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 51060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@rsu.su.cn.
FEATURES
Location/Qualifiers
1..490
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Alignment Scores:
Pred. No.: 7.1e-46 Length: 490
Score: 519.00 Matches: 98
Percent Similarity: 91.9% Conservative: 4
Best Local Similarity: 88.3% Mismatches: 9
Query Match: 88.3% Indels: 0
DB: 5 Gaps: 0

US-10-092-640-36 (1-111) x CD692216 (1-490)

QY 1 GlnSerValleuthrGlnProProSerValSerAlaAlaProGlyGlnysValThrIle 20
|||
Db 117 CACTGTGTGCTGACTGACCACTCAGCTCTGGAGCCCCGGGCGAGAGGTCACCATC 176
|||
QY 21 SerCySerGlySerSerSerSerAenllEgLYAsnAsnTYrValSerTPYrGlnGlnLeu 40
|||
Db 177 TCTTGCTCTGGAAGCAGCTTCATATGAAATATATATATGTAATGTCGACGACCACTC 236
|||
QY 41 ProGlyThrAlaProlyLeuLeuIleTYrGlyHisThrAsnArgProAlaGlyValPro 60
|||
Db 237 CCAGGAACGGCCCCCAAGCTCCATCTATAGGAACAATCAGCGACCTCAGGGGTCCT 296
|||
QY 61 AspArgPheSerGlySerlySerGlyThSerAlaSerLeuAlaIleSerGlyPheArg 80
|||
Db 297 GACCGATTCTCTGGCTCCAGTCTGACCTCAGCTCCCTGGCCATCAGTGCATCCGG 356
|||
QY 81 SerGluAspGluAlaAspTYrTYrCyAlaAlaIleTPAspAspSerLeuSerGlyTPVal 100
|||
Db 357 TCCGAGAGATGAGGCTGATATTATGTCAGCATGGATGACAGCTGAGTGGTGGTC 416
|||
QY 101 PheGlyGlyGlyThrlyLeuThrValLeuGly 111
|||
Db 417 TTCGGCGAGGAGCAAGCTGACCGTCTAGGT 449
|||

RESULT 4
DA992977 548 bp mRNA linear EST 03-DEC-2005
LOCUS DA992977 STNOVA Homo sapiens cDNA clone STNOV4005343 5', mRNA
DEFINITION sequence.
ACCESSION DA992977
VERSION DA992977.1 GI:83070668
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 548)

AUTHORS
Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,U., Sekine,M., Tsutitani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushiida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuna,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE
Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL
Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT
Contact: Takao Isogai
RIJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: fuj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
FEATURES
Location/Qualifiers
1..548
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="STNOV4005343"
/issue_type="synovial membrane tissue from rheumatoid arthritis"
/clone_lib="STNOV4"
/note="Vector: PME18SFL3"

ORIGIN
Alignment Scores:
Pred. No.: 1.53e-45 Length: 548
Score: 516.50 Matches: 99
Percent Similarity: 92.0% Conservative: 4
Best Local Similarity: 88.4% Mismatches: 8
Query Match: 87.8% Indels: 1
DB: 9 Gaps: 1

US-10-092-640-36 (1-111) x DA992977 (1-548)

QY 1 GlnSerValleuthrGlnProProSerValSerAlaAlaProGlyGlnysValThrIle 20
|||
Db 104 CACTGTGTGCTGACTGACCACTCAGCTCTGGAGCCCCGGGCGAGAGGTCACCATC 163
|||
QY 21 SerCySerGlySerSerSerSerAenllEgLYAsnAsnTYrValSerTPYrGlnGlnLeu 40
|||
Db 164 TCTTGCTCTGGAAGCAGCTTCATATGAAATATATATGTAATGTCGACGACCACTC 223
|||
QY 41 ProGlyThrAlaProlyLeuLeuIleTYrGlyHisThrAsnArgProAlaGlyValPro 60
|||
Db 224 CCAGGAACGGCCCCCAAGCTCCATCTATAGGAACAATCAGCGACCTCAGGGGTCCT 293
|||
QY 61 AspArgPheSerGlySerlySerGlyThSerAlaSerLeuAlaIleSerGlyPheArg 80
|||
Db 284 GACCGATTCTCTGGCTCCAGTCTGACCTCAGCTCCCTGGCCATCAGTGCATCCGG 343
|||
QY 81 SerGluAspGluAlaAspTYrTYrCyAlaAlaIleTPAspAspSerLeuSerGlyTPVal 99
|||
Db 344 TCCGAGAGATGAGGCTGATATTATGTCAGCATGGATGACAGCTGAGTGGTCTGG 403
|||
QY 100 ValPheGlyGlyGlyThrlyLeuThrValLeuGly 111
|||
Db 404 GTTTCGGCGAGGAGCAAGCTGACCGTCTAGGT 439
|||

RESULT 5
BX283265 494 bp mRNA linear EST 04-MAR-2003
LOCUS BX283265

```

DEFINITION   BX283265 NIH MGC 48 Homo sapiens cDNA clone IMAGE958D081707 ;
IMAGE:4856407, mRNA sequence.
ACCESSION    BX283265
VERSION      BX283265.1  GI:28847719
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 494)
REFERENCE    Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
COMMENT      Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69130 Heidelberg, Germany
RZPD; IMAGE958D081707.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection:
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/Cloncats/cgi-
bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
PCMW-M31u, Primer sequence: CGTGTGTAACGACGCGCACT.
Location/Qualifiers
1..494
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE958D081707 ; IMAGE:4856407"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1.51e-45 Length: 494
Score: 516.00 Matches: 99
Percent Similarity: 91.2% Conservative: 4
Best Local Similarity: 87.6% Mismatches: 8
Query Match: 87.8% Indels: 2
DB: 4 Gaps: 1

US-10-092-640-36 (1-111) x BX283265 (1-494)
QY 1 GInSeValleuThrGInProSeSerValSerAlaAlaProGlyGInLysValThrIle 20
|||||
Db 90 CAGTGTGTCCTAGCTACGACCACTCAGCGCTCGGAGACCCCGGAGAGGCGTCACTAC 149
|||||
QY 21 SerCySeSerGlySerSerSerSerAniIleGlyAsnAsnTyrValSerTrpTyrGInGlnLeu 40
|||||
Db 150 TCTGTGTTCTGAAGCAGCTCCAAACATCGGAAGTAATTATGTAATCTGTACACGACGCTC 209
|||||
QY 41 ProGlyThrAlaProLysLeuLeuLeuLeuTyrGlyHisThrAsnArgProAlaGlyValPro 60
|||||
Db 210 CCAGGAACGGCCGCCCAACTCTCATCTATAGGAATATATCAGCGCCCTCAGGCGCTCCT 269
|||||

```

```

QY 61 AsparGPeSeSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
|||||
Db 270 GACCACTTCTCTGGCTCCAGCTCTGACACTTACGCTCCCTGGCCATCATGTGGCTCCGG 329
|||||
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIlePASPASPSPSerLysSerGly----- 98
|||||
Db 330 TCCGAGGATGAGCGCTGATTATTACTGTGACATGGATGACAGCTGAGTGCCTCCAAAT 389
|||||
QY 99 TrpValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
|||||
Db 390 TGGGTGTTCTGGGAGGAGGACCAAGCTGACCTGCTCTAGGT 428
|||||

RESULT 6
BM314111
LOCUS      512 bp      mRNA      linear      EST 03-JUN-2002
DEFINITION ih07c03.y1 Human insulinoma Homo sapiens cDNA 5' similar to
SW:LVIG.HUMAN P06316 IG LAMBDA CHAIN V-I REGION BLZ PRECURSOR. ;
mRNA sequence.
BM314111
ACCESSION  BM314111.1  GI:18048456
VERSION     BM314111
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 512)
REFERENCE    Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvilli, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
COMMENT      Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1..512
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN
Alignment Scores:
Pred. No.: 1.59e-45 Length: 512
Score: 516.00 Matches: 96

```


Percent Similarity: 91.9% Conservative: 6
 Best Local Similarity: 86.5% Mismatches: 9
 Query Match: 87.8% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BM314111 (1-512)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
 |||
 DB 75 CAGTCTGTGCTGACTGACGACCCCTCAGCGCTGGGACCCCGGAGAGGTCACCATC 134
 |||
 QY 21 SerCysSerGlySerSerSerSerAenIleGlyAsnAsnTyValSerTPYrGlnGlnLeu 40
 |||
 DB 135 TCTTGTTCGGAAGCAGCTCCACATCGCGGTAATCATGTACCTGTACCAATC 194
 |||
 QY 41 ProGlyThrAlaProLyLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
 |||
 DB 195 CCAGGAACGGCCCCCAAAATCTCATCTATAGAAATAATCAGCGGCGCTCAGGGGTCCT 254
 |||
 QY 61 AspArgPheSerGlySerSerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 |||
 DB 255 GACCGATTCTCCGGCTCCAAAGTCTGGCAGCTCAGCCCTCCCTGGCCATCAGTGCCTCGG 314
 |||
 QY 81 SerGluAspGluAlaAspTYrTYrCYsAlaAlaTrpAspAspSerLeuSerGlyTPYrVal 100
 |||
 DB 315 TCCGAGATGAGGCTGATTTACTGTGCGAGCATGGATGACAGCTGAGTGTGGGTG 374
 |||
 QY 101 PheGlyGlyGlyThrTyLeuThrValLeuGly 111
 |||
 DB 375 TTCGGCGGAGGACCAAGTGCAGCTGCTTGGT 407
 |||

RESULT 7
 BG755949 656 bp mRNA linear EST 15-MAY-2001
 LOCUS 602716426F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856407 5',
 mRNA sequence.

ACCESSION BG755949
 VERSION BG755949.1 GI:14066602
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

1 (bases 1 to 656)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staude, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LNCM1707 row: d column: 08

High quality sequence stop: 654.

Location/Qualifiers

1. 656

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4856407"

/tissue type="primary B-cells from tonsils (cell line)"

/lab host="DH10B (phage-resistant)"

/clone lib="NIH_MGC_48"

/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
 Site: 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using
 the following 5' adaptor: GGACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-45 Length: 656
 Score: 516.00 Matches: 99
 Percent Similarity: 91.2% Conservative: 4
 Best Local Similarity: 87.6% Mismatches: 8
 Query Match: 87.8% Indels: 2
 DB: 2 Gaps: 1

US-10-092-640-36 (1-111) x BG755949 (1-656)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
 |||
 DB 90 CAGTCTGTGCTGACTGACGACCCCTCAGCGCTGGGACCCCGGAGAGGTCACCATC 149
 |||
 QY 21 SerCysSerGlySerSerSerSerAenIleGlyAsnAsnTyValSerTPYrGlnGlnLeu 40
 |||
 DB 150 TCTTGTTCGGAAGCAGCTCCACATCGGAAATATATGTATACCTGTACCAAGCTC 209
 |||
 QY 41 ProGlyThrAlaProLyLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValPro 60
 |||
 DB 210 CCAGGAACGGCCCCCAAACTCTCATCTATAGAAATAATCAGCGGCGCTCAGGGGTCCT 269
 |||
 QY 61 AspArgPheSerGlySerSerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 |||
 DB 270 GACCGATTCTCCGGCTCCAAAGTCTGGCAGCTCAGCCCTCCCTGGCCATCAGTGCCTCGG 329
 |||
 QY 81 SerGluAspGluAlaAspTYrTYrCYsAlaAlaTrpAspAspSerLeuSerGly----- 98
 |||
 DB 330 TCCGAGATGAGGCTGATTTACTGTGCGAGCATGGATGACAGCTGAGTGTGGGTG 389
 |||
 QY 99 TrpValPheGlyGlyGlyThrTyLeuThrValLeuGly 111
 |||
 DB 390 TGGGTGTCGGCGGAGGACCAAGTGCAGCTGCTTGGT 428
 |||

RESULT 8

DA978161 552 bp mRNA linear EST 15-NOV-2005
 LOCUS DA978161 SYN0V2 Homo sapiens cDNA clone SYN0V2009255 5', mRNA
 sequence.

DEFINITION

ACCESSION

DA978161 GI:82436709

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT

FLJ Project

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEBO human cDNA project (New Energy and Industrial Technology

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES
source
1. 552
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SYNOV2009255"
/tissue_type="synovial membrane tissue from rheumatoid arthritis"
/clone_lib="SYNOV2"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 1,98e-45 Length: 552
Score: 515.50 Matches: 99
Percent Similarity: 91.1% Conservative: 9
Best Local Similarity: 88.4% Mismatches: 1
Query Match: 87.7% Indels: 1
DB: 9 Gaps: 1

US-10-092-640-36 (1-111) x DA978161 (1-552)

QY 1 GlnSerValLeuThrGlnProPseValSerAlaAlaProGlyGlnLysValThrIle 20
DB 104 CAGTGTGCTGCTACCTCAGCACCCTCAGCGCTGGAGGCCCGGAGAGGGTCAACATC 163
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 164 TCTTGTCTCGAAGCAGCTCCACATCAGAAATATTAATGCTCTCTGTAACAGCAGCTC 223
QY 41 ProGlyThrAlaProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 224 CCAGGAAGGGCCCCCAACTCCTCATCTATGAAATATCAGAGGCGCTCAGAGGCTCCT 283
QY 61 AspArgPheSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 80
DB 284 GACCGATTCTCGGCTCCCAAGCTGGCAGCTCAGCTCCCTGGCCATCAGTGGCTCCGG 343
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTTPAspAspSerLeuSerGly--TTP 99
DB 344 TCCGAGATGAGGCTCTTATTAATGTCACATGAGATGACAGCTGAGTGTCTCTTGG 403
QY 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
DB 404 GTGTCGGCGAGGAGCAAGCTGACGCTCTAGGT 439

RESULT 9

LOCUS

BG686011 873 bp mRNA linear EST 01-MAY-2001
602638561F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766295 5',
mRNA sequence.

DEFINITION

ACCESSION

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 873)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis W. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1626 row: 1 column: 16
High quality sequence stop: 842.

FEATURES
source
1. 873
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4766295"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOT7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 8.54e-45 Length: 873
Score: 512.00 Matches: 95
Percent Similarity: 91.9% Conservative: 7
Best Local Similarity: 85.6% Mismatches: 9
Query Match: 87.1% Indels: 0
DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BG686011 (1-873)

QY 1 GlnSerValLeuThrGlnProPseValSerAlaAlaProGlyGlnLysValThrIle 20
DB 88 CAGTGTGCTGCTACCTCAGCACCCTCAGCGCTGGAGGCCCGGAGAGGGTCAACATC 147
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 148 TCTTGTCTCGAAGCAGCTCCCAACATCGAATATTAATGTAACCTGTAACAGCAGCTC 207
QY 41 ProGlyThrAlaProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 208 CCAGGAAGGGCCCCCAACTCCTCATCTATGAAATATCAGAGGCGCTCAGAGGCTCCT 267
QY 61 AspArgPheSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 80
DB 268 GACCGATTCTCGGCTCCCAAGCTGGCAGCTCAGCTCCCTGGCCATCAGTGGCTCCGG 327
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTTPAspAspSerLeuSerGlyTTPVal 100
DB 328 TCTGAGATGAGGCTGATTAATTAATGTCACAGATGAGATGACAGCTGATGTTGGTG 387
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
DB 388 TTGCGGAGGAGGAGCAAGCTGACGCTCTAGGT 420

RESULT 10

LOCUS

BG535669 780 bp mRNA linear EST 03-APR-2001
602633799F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4688082 5',
mRNA sequence.

DEFINITION

ACCESSION

KEYWORDS

EST.

SOURCE

ORGANISM

1 (bases 1 to 780)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis W. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

REFERENCE 1 (bases 1 to 780)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LICM1501 row: n column: 19
 High quality sequence stop: 707.

FEATURES

source
 1. 780
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:468082"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1lb="NIH_MGC_77"
 /note="Organism: lung; Vector: pDNR-LIB (Clontech); Site: 1;
 SfiI (ggcgccctcgcc); Site 2: SfiI (ggcgccatgagcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCGCATTTATGGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCCGAGCGCCGACATC-3' (30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 9,48e-45 Length: 780
 Score: 511.00 Matches: 96
 Percent Similarity: 91.0% Conservative: 5
 Best Local Similarity: 86.5% Mismatches: 10
 Query Match: 86.9% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BG535669 (1-780)

QY 1 GInSeRVaIlleuThInPrOseRVaISerAlaLaPrOgLyInLySValThrIle 20
 Db 105 CAGTCTGTGCTGACTCAGCCACCTCAGCGTGGAGCCCGGAGAGGTCACCATC 164
 QY 21 SerCySeSerGlySerSerSerAnIlleGlyAsnAsnTyValSerTrpTyrgInGInleu 40
 Db 165 TCTTGTTCGGAAGCACTCCAACTCGGAAGTAACTGTAATACGTAACCGCAATTC 224
 QY 41 ProGlyThAlaProLyLeuLeuIleTyrgLyHISThrAsnArgProAlaGlyValPro 60
 Db 225 CCAAGAACGGCCCCCAAACTCTCATCTATAGAAATATAGCGGCCCTTAGGGGTCCT 284
 QY 61 AspArgPhSeSerGlySerLySerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 285 GACCGATTCTCTGGCTCCAAAGTCTGGACCTCAGCTCCCTGACATCACTGGGTCCTCG 344
 QY 81 SerGluAspGluAlaAspTrpTyrgValAlaIleTrpAspAspSerLeuSerGlyTrpVal 100
 Db 345 TCCGAGGATGAGGCTAATTATTACTGTGAGCATGGAGATGACAGCTGAGTGGGTGGTG 404
 QY 101 PheGlyGlyGlyThrLyLeuThrValLeuGly 111
 Db 405 TTCGGCGAGGAGCAAGCTGACCTCTTAGGT 437

RESULT 11
 DA971136 566 bp mRNA linear EST 11-NOV-2005
 LOCUS DA971136
 DEFINITION DA971136 SYNOV2 Homo sapiens cdna clone SYNOV2000476 5', mRNA

ACCESSION DA971136
 VERSION DA971136.1
 KEYWORDS GI:82082025
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE

1 (bases 1 to 566)
 Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsutitani,K., Wakaguni,H.,
 Ichi,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kuchida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuna,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 JOURNAL PUBMED
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3966
 Email: flj-cdna@flj.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan): cDNA library construction:
 Helix Research Institute (HRI), 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.

TITLE

FEATURES

source
 1. 566
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SYNOV2000476"
 /tissue_type="synovial membrane tissue from rheumatoid
 arthritis"
 /clone_1lb="SYNOV2"
 /note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 1,03e-44 Length: 566
 Score: 509.00 Matches: 95
 Percent Similarity: 91.9% Conservative: 7
 Best Local Similarity: 85.6% Mismatches: 9
 Query Match: 86.6% Indels: 0
 DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x DA971136 (1-566)

QY 1 GInSeRVaIlleuThInPrOseRVaISerAlaLaPrOgLyInLySValThrIle 20
 Db 105 CAGTCTGTGCTGACTCAGCCACCTCAGCGTGGAGCCCGGAGAGGTCACCATC 164
 QY 21 SerCySeSerGlySerSerSerAnIlleGlyAsnAsnTyValSerTrpTyrgInGInleu 40
 Db 165 TCTTGTTCGGAAGCACTCCAACTCGGAAGTAACTGTAATACGTAACCGCAATTC 224
 QY 41 ProGlyThAlaProLyLeuLeuIleTyrgLyHISThrAsnArgProAlaGlyValPro 60
 Db 225 CCAAGAACGGCCCCCAAACTCTCATCTTATAGAAATATAGCGGCCCTTAGGGGTCCT 284
 QY 61 AspArgPhSeSerGlySerLySerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 Db 285 GACCGATTCTCTGGCTCCAAAGTCTGGACCTCAGCTCCCTGACATCACTGGGTCCTCG 344
 QY 81 SerGluAspGluAlaAspTrpTyrgValAlaIleTrpAspAspSerLeuSerGlyTrpVal 100

```

Db      345 TCTGAGGATGAGCGCTGATTATTACTGTGAGCTTGAGGACAGCCTGAAATGGTTGGGTG 404
QY      101 Phegiylgylgylthrlsleuthrvalleugly 111
Db      405 TTCGGCGGAGGAGCCAGCTGACCGCTCCAGGT 437

RESULT 12
DA920210
LOCUS   DA920210 SMINT2 Homo sapiens cDNA clone SMINT2005585 5', mRNA
DEFINITION
sequence.
ACCESSION DA920210
VERSION   DA920210
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homidae; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS   Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
          Yamashita, R., Yamamoto, D., Sekine, M., Tsuritani, K., Wakaquri, H.,
          Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
          Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
          Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
          Tanabe, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
          Diversification of Transcriptional Modulation: Large-scale
          Identification and Characterization of Putative Alternative
          Promoters of Human Genes
JOURNAL   Genome Res. 16 (1), 55-65 (2006)
PUBMED    16344560
COMMENT   Contact: Takao Isogai
          FLJ Project (HRI Team)
          Helix Research Institute
          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: flj-cdna@nifty.com
          NEDO human cDNA project (New Energy and Industrial Technology
          Developmental Organization, Japan); cDNA library construction:
          Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
          Research Association for Biotechnology (RAB) and Biotechnology
          Center, National Institute of Technology and Evaluation; 3'-end one
          pass sequencing: RAB.
FEATURES
         source             1..578
         location/Qualifiers
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="SMINT2005585"
         /tissue_type="small intestine"
         /clone_lib="SMINT2"
         /note="Vector: PME18SFL3"

ORIGIN
Alignment Scores:
Pred. No.:      1.06e-44      Length:      578
Score:          509.00      Matches:      97
Percent Similarity: 91.0%      Conservative: 4
Best Local Similarity: 87.4%      Mismatches: 10
Query Match:    86.6%      Indels:      0
DB:            9      Gaps:      0

US-10-092-640-36 (1-111) x DA920210 (1-578)
QY      1 GlnSerValleuThrGlnProPseSerValSerAlaAlaProGlyGlnIlyValThrIle 20
Db      102 CAGTGTGTCTACTAGCACCCTCAGGCTCTGGAGACCCCGGCGAGAGGGTCCACCATC 161
QY      21 SerCySerGlySerSerSerAnillegIAsnAsnIlyrValSerTrpTyrglnIleu 40
Db      162 TCTTGTTCGGAGAGCTCCAAACATCGGAATAATATATAGTACTGTGTACAGCACTC 221

```

```

QY      41 ProGlyThrAlaProIlyleuIleuIleTyrglyHisThrAsnArgProAlaIlyValPro 60
Db      222 CCAGAGAGGCGCCCCCAACTCCTCATCTATATAGTATCAGCGGCGCTCAGGGGTCCCT 281
QY      61 AspArgPheSerGlySerIlySerGlyThrSerAlaSerIleuAlIleSerGlyPheArg 80
Db      282 GACCATTTCTCTGGCTCCAGCTCGACCTCAGCTCCCTGGCCATCATGTGGCTCCGG 341
QY      81 SerGluAspGluAlaAspTyTrTyrcysAlaAlaIATpAspAspSerIleuSerGlyTrpVal 100
Db      342 TCCGAGGATGAGGCTAATATTAATTAATGTCAGATGGAGTACAGCCTGACTGTGTGGTG 401
QY      101 Phegiylgylgylthrlsleuthrvalleugly 111
Db      402 TTCGGCGGAGGAGCCAGCTGACGTCCTCGGT 434

RESULT 13
DN998001
LOCUS   DN998001 620 bp mRNA linear EST 17-MAY-2005
DEFINITION TC103037 Human breast cancer tissue, large insert, PCMV expression
          library Homo sapiens cDNA clone TC103037 5', similar to Homo
          sapiens, clone WGC:32654 IMAGE:4701898, complete cds, mRNA
          sequence.
ACCESSION DN998001
VERSION   DN998001.1 GI:66257828
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homidae; Homo.
REFERENCE 1 (bases 1 to 620)
AUTHORS   Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
          Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
          Zhang, X., Jay, G. and He, W.
          High-throughput cloning of full-length human cDNAs directly from
          cDNA libraries optimized for large and rare transcripts
JOURNAL   Unpublished (2005)
COMMENT   Contact: Kovacs, KP
          High Throughput cDNA Cloning
          Origene Technologies, Inc. ( www.origene.com )
          6 Taft Court, Suite 100, Rockville, MD 20850, USA
          Tel: 301 340 3188
          Fax: 301 340 8606
          Email: cDNA@origene.com
          This EST submission is part of an on-going human full-length
          cloning project at Origene Technologies, Inc.
          Please contact Origene for access.
          Origene Technologies, Inc.
          6 Taft Ct. Suite 100
          Rockville, MD 20850
          Tel: (301) 340-3188
          http://www.origene.com
          Seq primer: PCMV6 prime forward vector primer, Origene
          Technologies Inc.
FEATURES
         source             1..620
         location/Qualifiers
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="TC103037"
         /tissue_type="breast cancer"
         /clone_lib="Human breast cancer tissue, large insert, PCMV
         expression library"
         /note="Organ: Mammary gland (cancer tissue); Vector:
         PCMV6-Xb5; Site 1: EcoRI; Site 2: XhoI/Sall compatible end
         ligatio; Oligo-dT primed reverse transcription optimized
         for large and GC rich mRNA transcripts, cDNA size
         selection, optimized ligation for large inserts into
         mammalian expression vector, random clones selected for
         end sequence verification of full-length genes"

ORIGIN

```

Alignment Scores:

Pred. No.: 1.16e-44 Length: 620
 Score: 509.00 Matches: 95
 Percent Similarity: 91.9% Conservative: 7
 Best Local Similarity: 85.6% Mismatches: 9
 Query Match: 86.6% Indels: 0
 DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x DN988001 (1-620)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
 |||||
 DB 91 CAGTCTGTCTGACTGACCCACCTTCAGCTCTGGAGCCCGGAGAGGATCACCATC 150
 |||||
 QY 21 SerCysSerGlySerSerSerSerSerSerValSerValSerTyrGlnGlnLeu 40
 |||||
 DB 151 TCTTGTCTTGGAGAGAGCTCCGACATCGAAGATATATATATGTTCCAGCAGCTC 210
 |||||
 QY 41 ProGlyThrAlaProIleuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
 |||||
 DB 211 CCGAGAACGGCCCCCAAACTCCATCTATAGAAATATATCAGCGCCCTCAGGGGTCCT 270
 |||||
 QY 61 AspArgPheSerGlySerSerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 |||||
 DB 271 GACCGATTCTCTGGCTCCAGCTCCGACCTCCCTCCGACATCAGTGGCTCCGG 330
 |||||
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTyrAspAspSerLeuSerGlyTyrVal 100
 |||||
 DB 331 TCCGAGATGAGGCTGATTTATCTGTGATCATGAGATGACAGCTGAGCTGCTGGGTG 390
 |||||
 QY 101 PheGlyGlyGlyThrIleLeuThrValLeuGly 111
 |||||
 DB 391 TTCGGCGAGGAGCAAGCTGACCTGCTTAGGT 423

RESULT 14
 LOCUS BG745508 680 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602724089F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850231 5',
 mRNA sequence.

ACCESSION BG745508
 VERSION BG745508.1 GI:14056161
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 680)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-rc@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM691 row: b column: 24
 High quality sequence stop: 678.

FEATURES

source

1..680
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4850231"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 113"
 /note="Organ: spleen; Vector: pONB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned

ORIGIN

Alignment Scores:

Pred. No.: 1.31e-44 Length: 680
 Score: 509.00 Matches: 97
 Percent Similarity: 90.1% Conservative: 3
 Best Local Similarity: 87.4% Mismatches: 11
 Query Match: 86.6% Indels: 0
 DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x BG745508 (1-680)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
 |||||
 DB 89 CAGTCTGTCTGACTGACCCACCTTCAGCTCTGGAGCTCCCGGAGAGGATCACCATC 148
 |||||
 QY 21 SerCysSerGlySerSerSerSerSerValSerValSerTyrGlnGlnLeu 40
 |||||
 DB 149 TCTTGTCTTGGAGAGAGCTCCACATCGAATATATATATATGTTACCAAGACTC 208
 |||||
 QY 41 ProGlyThrAlaProIleuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
 |||||
 DB 209 CCGAGAACGGCCCCCAAACTCCATCTATCAGAAATATATCAGCGCCCTCAGGGGTCCT 268
 |||||
 QY 61 AspArgPheSerGlySerSerSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
 |||||
 DB 269 GACCGATTCTCTGGCTCCAGCTCCGACCTCCCTCCGACATCAGTGGCTCCGG 328
 |||||
 QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTyrAspAspSerLeuSerGlyTyrVal 100
 |||||
 DB 329 TCCGAGATGAGGCTGATTTATCTGTGATCATGAGATGACAGCTGAGTCTGGGTG 388
 |||||
 QY 101 PheGlyGlyGlyThrIleLeuThrValLeuGly 111
 |||||
 DB 389 TTCGGCGAGGAGCAAGCTGACCTGCTTAGGT 421

RESULT 15

LOCUS AM405612 498 bp mRNA linear EST 16-FEB-2000
 DEFINITION UI-HF-BL0-abs-b-11-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
 IMAGE:3057381 5', mRNA sequence.

ACCESSION AM405612
 VERSION AM405612.1 GI:6924669
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 498)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-rc@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward.

FEATURES

source

1..498
 /organism="Homo sapiens"

into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 17:06:37 ; Search time 144.3 Seconds
(without alignments)
2158.972 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588
Sequence: 1 QSVLTPSPVSAAPGQKVTI.....WDSLSEGVFGSGTKTLTVLG 111

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 segs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q/abs/ABSSMBE.spool/US10092640/runat.25052006.155719.5922/app.query.fasta_1
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPLC=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humano0.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs020h -USER=US10092640@CGN 1 1 252 @runat.25052006.155719.5922
-NCPU=6 -ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588	100.0	774	2	US-08-665-202-4
2	588	100.0	774	3	US-09-315-574-4
3	516	87.8	908	3	US-09-273-839A-9
4	508	86.4	327	3	US-09-240-274-128
5	508	86.4	327	3	US-09-848-798-128
6	504	85.7	333	3	US-09-424-840B-7
7	486	82.7	333	2	US-08-264-093-5
8	486	82.7	333	2	US-08-477-553A-43

9	480	81.6	327	3	US-09-240-274-129	Sequence 129, App
10	480	81.6	327	3	US-09-848-798-129	Sequence 129, App
11	477.5	81.2	336	2	US-08-345-321-3	Sequence 3, Appl1
12	477.5	81.2	935	3	US-09-049-672A-20	Sequence 20, Appl1
13	476	81.0	327	3	US-09-240-274-124	Sequence 124, App
14	476	81.0	327	3	US-09-848-798-124	Sequence 124, App
15	476	81.0	705	3	US-09-372-425A-3	Sequence 3, Appl1
16	471	80.1	327	3	US-09-240-274-130	Sequence 130, App
17	471	80.1	327	3	US-09-848-798-130	Sequence 130, App
18	471	80.1	585	3	US-09-620-312D-551	Sequence 551, App
19	469	79.8	327	3	US-09-240-274-126	Sequence 126, App
20	469	79.8	327	3	US-09-848-798-126	Sequence 126, App
21	468	79.6	342	3	US-09-240-274-131	Sequence 131, App
22	468	79.6	342	3	US-09-848-798-131	Sequence 131, App
23	466	79.3	336	3	US-10-153-437-2	Sequence 2, Appl1
24	466	79.3	895	3	US-09-049-672A-25	Sequence 25, Appl1
25	466	79.3	5079	3	US-09-809-517A-41	Sequence 41, Appl1
26	465	79.1	330	2	US-08-199-911-1	Sequence 1, Appl1
27	463	78.7	915	4	US-09-880-107-3743	Sequence 3743, App
28	462	78.6	333	2	US-08-652-816A-27	Sequence 27, Appl1
29	458	77.9	333	2	US-10-072-301A-26	Sequence 26, Appl1
30	457.5	77.8	333	2	US-08-305-683A-3	Sequence 3, Appl1
31	454	77.2	327	3	US-09-025-769B-50	Sequence 50, Appl1
32	454	77.2	327	3	US-09-490-070A-50	Sequence 50, Appl1
33	454	77.2	327	3	US-09-490-153-50	Sequence 50, Appl1
34	454	77.2	327	3	US-09-490-324-50	Sequence 50, Appl1
35	451.5	76.8	933	3	US-09-079-029-8	Sequence 8, Appl1
36	450	76.5	327	3	US-09-240-274-123	Sequence 23, App
37	450	76.5	327	3	US-09-848-798-123	Sequence 23, App
38	446.5	75.9	1005	3	US-09-646-028-41	Sequence 41, Appl1
39	446.5	75.9	1020	3	US-09-646-028-44	Sequence 44, Appl1
40	446.5	75.9	1047	3	US-09-646-028-47	Sequence 47, Appl1
41	445	75.7	327	3	US-09-240-274-125	Sequence 125, App
42	445	75.7	327	3	US-09-848-798-125	Sequence 125, App
43	444.5	75.6	330	3	US-09-240-274-132	Sequence 132, App
44	444.5	75.6	330	3	US-09-848-798-132	Sequence 132, App
45	440	74.8	327	3	US-09-240-274-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-665-202-4
; Sequence 4, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995

```
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION:
OTHER INFORMATION: antibody C6.5"
US-08-665-202-4

Alignment Scores:
Pred. No.: 7,98e-58 Length: 774
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-092-640-36 (1-111) x US-08-665-202-4 (1-774)

QY 1 GlnSerValLeuThGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
Db 433 CAGTCTGTGTTGACGACGCGCCCTCAGTGTGCGGCCCGACGACAGAGGTCAACCATC 492
QY 21 SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnTrpValSerTrpTrpGlnGlnLeu 40
Db 493 TCCTGCTCTGGAAGGAGCTCCAACTGGGAATTAATTAATTAATTAATTAATTAATTAATTA 552
QY 41 ProGlyThrAlaProLysLeuLeuIleTrpGlyHisThrAsnArgProAlaGlyValPro 60
Db 553 CCAGGAACAGCCCCCAACTCTCATCTATGTGTACACCAATCGCGCCGAGGGGTCCCT 612
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db 613 GACCGATTCTTGCTGCTCCAGTCTGACACCTGACCTCCCTGCGCATCGAGGTTCGG 672
QY 81 SerGluAspGluAlaAspTrpTrpCysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100
Db 673 TCCGAGATGAGGCTGATTATTACTGTGACGATGGATGACAGCTGAGTGTGGGTG 732
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 733 TTCGGCGGAGGAGCAACGCTGACCGTCTAGGT 765

RESULT 2
US-09-315-574-4
Sequence 4, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSER: Majestic, Parsons, Siebert & Heue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
OTHER INFORMATION:
OTHER INFORMATION: antibody C6.5"
US-09-315-574-4

Alignment Scores:
Pred. No.: 7,98e-58 Length: 774
Score: 588.00 Matches: 111
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-315-574-4 (1-774)

QY 1 GlnSerValLeuThGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
Db 433 CAGTCTGTGTTGACGACGCGCCCTCAGTGTGCGGCCCGACGACAGAGGTCAACCATC 492
QY 21 SerCysSerGlySerSerSerSerAsnIleGlyAsnAsnTrpValSerTrpTrpGlnGlnLeu 40
Db 493 TCCTGCTCTGGAAGGAGCTCCAACTGGGAATTAATTAATTAATTAATTAATTAATTAATTA 552
QY 41 ProGlyThrAlaProLysLeuLeuIleTrpGlyHisThrAsnArgProAlaGlyValPro 60
Db 553 CCAGGAACAGCCCCCAACTCTCATCTATGTGTACACCAATCGCGCCGAGGGGTCCCT 612
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db 613 GACCGATTCTTGCTGCTCCAGTCTGACACCTGACCTCCCTGCGCATCGAGGTTCGG 672
QY 81 SerGluAspGluAlaAspTrpTrpCysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100
Db 673 TCCGAGATGAGGCTGATTATTACTGTGACGATGGATGACAGCTGAGTGTGGGTG 732
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 733 TTCGGCGGAGGAGCAACGCTGACCGTCTAGGT 765

RESULT 3
```



```
US-09-273-839A-9
; Sequence 9, Application US/09273839A
; Patent No. 632916
; GENERAL INFORMATION:
; APPLICANT: Cirino, Nick M
; APPLICANT: Jackson, Paul J
; APPLICANT: Lehnert, Bruce E
; TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
; FILE REFERENCE: S-89,662
; CURRENT APPLICATION NUMBER: US/09/273,839A
; CURRENT FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-273-839A-9

Alignment Scores:
Pred. No.: 1,63e-49 Length: 908
Score: 516.00 Matches: 98
Percent Similarity: 93.7% Conservative: 6
Best Local Similarity: 88.3% Mismatches: 7
Query Match: 87.8% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-273-839A-9 (1-908)
QY 1 GlnSerValLeuThrGlnProPheSerValSerAlaAlaProGlyGlnValThrIle 20
DB 505 CAGTCGTGTGTGCGAACCGCCCTCAGCCTCGGAGACCCCGGAGAGGTCACCATC 564
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
DB 565 TCTGTGTTCGGAAGCAGCTCCACATCGAAGATATTCCTTAACGTGATCCAGCAGCTC 624
QY 41 ProGlyThrAlaProIleuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60
DB 625 CAGGAAACCGCCCAACTCCCTCATCTATAGTAACAGCAATCGCCCTCAGGGGTCCT 684
QY 61 AsparGpHeSerGlySerIleuSerSerSerSerSerSerSerSerSerSerSerSer 80
DB 685 GACCGATCTCTGGCTCCAACTGCGACCTCAGCCCTCCCTGCGCATGAGTCCCG 744
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleuAspAspSerSerSerSerSer 100
DB 745 TCCGAGGATGAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 804
QY 101 PheGlyGlyGlyThrIleuThrValIleuGly 111
DB 805 TTCGGCGAGGAGCCAACTGACCGCTGAGTGTGCGGTG 804

RESULT 4
US-09-240-274-128
; Sequence 128, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 128
; LENGTH: 327
```

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain M02
US-09-240-274-128

Alignment Scores:
Pred. No.: 3,27e-49 Length: 327
Score: 508.00 Matches: 95
Percent Similarity: 92.5% Conservative: 4
Best Local Similarity: 88.8% Mismatches: 8
Query Match: 86.4% Indels: 0
DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-240-274-128 (1-327)
QY 4 LeuThrGlnProPheSerValSerAlaAlaProGlyGlnValThrIleSerCysSer 23
DB 7 CTCACGACGCCGCCCTCAGCGTGGAGACCCCGGAGAGGTCACCATCTTGTCTT 66
QY 24 GlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 43
DB 67 GGAAGCAGCTCCAACTCGAAGATATTAATTAATTAATTAATTAATTAATTAATTAAT 126
QY 44 AlaProIleuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 63
DB 127 GCCCCCAACTCTCATCTATAGAAATTAATCAACGCCCTCAGGGGTCTCCAGCAATTC 186
QY 64 SerGlySerIleuSerGlyThrSerAlaSerIleuAlaIleuSerGlyPheArgSerGlu 83
DB 187 TCTGGCTCCAACTGCGACCTCAGCTCCCTCCCTCATCATGAGGCTCCGCTCGAGAT 246
QY 84 GluAlaAspTyrTyrCysAlaAlaIleuAspAspSerSerSerSerSerSerSerSer 103
DB 247 GAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 306
QY 104 GlyThrIleuThrValIleu 110
DB 307 GGGACCAAGCTGACCGTCTTA 327

RESULT 5
US-09-848-798-128
; Sequence 128, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 128
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain M02
US-09-848-798-128

Alignment Scores:
Pred. No.: 3,27e-49 Length: 327
Score: 508.00 Matches: 95
Percent Similarity: 92.5% Conservative: 4
Best Local Similarity: 88.8% Mismatches: 8
Query Match: 86.4% Indels: 0
DB: 3 Gaps: 0
```

US-10-092-640-36 (1-111) x US-09-848-798-128 (1-327)

```
OY 4 LeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIleSerCysSer 23
    |||
DB 7 CTCAGCGACGCCCTCTACGCTCTGGGACCCCGGGCAGAGGGTCCACCTCTCTGTTCT 66
OY 24 GlySerSerSerAsnIleGlyAsnAsnValSerTrpTyGlnGlnLeuProGlyThr 43
    |||
DB 67 GGAAGACGCTCCAACTCGAAGTATTTGTTATTTGTTACGACGCTCCAGAGACG 126
OY 44 AlaProLysLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValProAspArgPhe 63
    |||
DB 127 GCCCCCAAACTCTCATCTATAGAAATATTCAGCGGCCCTCAGGGGTCCCTGACCGATTTC 186
OY 64 SerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGluAsp 83
    |||
DB 187 TCTGGCTCCAACTCGGACCTCAGGCTCCCTGGCCATCAGGGGCTCGGTCGCGAGAT 246
OY 84 GluAlaAspTyTrpCysAlaAlaTrpAspAspSerLeuSerGlyTrpValPheGlyGly 103
    |||
DB 247 GAGGCTGATTATTACTGTGACAGATGATGACGCTTAGTGTTGGGTTCGCGGGA 306
OY 104 GlyThrLysLeuThrValLeu 110
    |||
DB 307 GGGACCAAGCTGACCGTCTCTA 327
```

RESULT 6

US-09-424-840B-7
; Sequence 7, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-CEP1B/111A RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 7
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(333)
; OTHER INFORMATION:
US-09-424-840B-7

Alignment Scores:

Pred. No.: 9.6e-49 Length: 333
Score: 504.00 Matches: 93
Percent Similarity: 92.7% Conservatve: 8
Best Local Similarity: 85.3% Mismatches: 8
Query Match: 85.7% Indels: 0
Gaps: 0

US-10-092-640-36 (1-111) x US-09-424-840B-7 (1-333)

```
OY 3 ValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIleSerCys 22
    |||
DB 1 GTGGTACTCAGGACCTCTCAGGCTCTGGGACCCCGGGCAGAGGGTCCACCTCTCTTGT 60
OY 23 SerGlySerSerSerAsnIleGlyAsnAsnValSerTrpTyGlnGlnLeuProGly 42
    |||
DB 61 TCTGGAAGACGCTCCAACTCGAAGTATTTGTTAACTGTGATCCAGACGCTCCACAGA 120
```

```
OY 43 ThrAlaProLysLeuLeuIleTyGlyHisThrAsnArgProAlaGlyValProAspArg 62
    |||
DB 121 ACGGCCCAAACTCTCATCTATAGTATATATACGCGGCCCTCAGGGGTCTCTGACCGA 180
OY 63 PheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGlu 82
    |||
DB 181 TTCTGTGCTCCAACTCGGACCTCCTCAGGCTCCCTGGCCATCAGTGGGCTCCAGTCTGAG 240
OY 83 AspGluAlaAspTyTrpCysAlaAlaTrpAspAspSerLeuSerGlyTrpValPheGly 102
    |||
DB 241 GATGAGGCTGATTATTACTGTGACAGATGATGACGCTGAAATGTTGGGTTCGCGC 300
OY 103 GlyGlyThrLysLeuThrValLeuGly 111
    |||
DB 301 GGAGGACCAAGCTGACCGTCTCTAGCT 327
```

RESULT 7

US-08-264-093-5
; Sequence 5, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-264-093-5

Alignment Scores:

Pred. No.: 1.09e-46 Length: 333
Score: 486.00 Matches: 92
Percent Similarity: 89.2% Conservatve: 7
Best Local Similarity: 82.9% Mismatches: 12
Query Match: 82.7% Indels: 0
Gaps: 0

US-10-092-640-36 (1-111) x US-08-264-093-5 (1-333)

```
OY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
    |||
DB 1 CAGTGTGTGCTGACTCAGCACCTCTCAGGCTCTGGGACCCCGGGCAGAGGGTCCACATC 60
```


Db 238 GACCATCTCTGCTCCAGAGTCGACGACCCCTGGGCGATCAGCAGCTCAG 297
 QY 81 SerGlaSpGluAlaAspTyrCysAlaAlaTTPaspAspSerLeuSergly---Tyr 99
 Db 298 ACTGGGAGACAGCGCCGATTTCTCTGGCAACATGGGATAGCGCCCTGAGTGG 357
 QY 100 ValPheGlyGlyGlyThrLeuThrValLeu 110
 Db 358 GTCTTCGGCGAGGAGCAAGCTGACCGCTCTTA 390

RESULT 12
 US-09-049-672A-20
 ; Sequence 20, Application US/09049672A
 ; Patent No. 6135941
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/049,672A
 ; FILING DATE: HERewith
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ceirone, Michael C
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PF-0497 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 935 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: ADREUT05
 ; CLONE: 2492122
 ; US-09-049-672A-20

Alignment Scores:
 Pred. No.: 4.19e-45 Length: 935
 Score: 477.50 Matches: 93
 Percent Similarity: 90.2% Conservative: 8
 Best Local Similarity: 83.0% Mismatches: 10
 Query Match: 81.2% Indels: 1
 DB: 3 Gaps: 1

US-10-092-640-36 (1-111) x US-09-049-672A-20 (1-935)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIle 20
 Db 131 CAGCTGTGTGACGAGCGCCCTCAGTCTGGGGCCCGAGGAGGATCACCATC 190
 QY 21 SerCysSerGlySerSerSerSerAlaIleGlyAsnAsnTyr---ValSerTyrGlnGln 39
 Db 191 TCCTGACACTGGGAGGAGCTCCACATCGGGGAGGTTATATATACCTGATCAGTACAGAG 250
 QY 40 LeuProGlyThrAlaProLeuLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
 Db 251 CTTCAGGAACAGCCCCCAAACTCCATCATATAGTAGTAAGAAATGGCCCTCAGGAGTCT 310
 QY 60 ProAspArgPheSerGlySerGlySerGlyThrSerAlaSerLeuAlaIleSerglyPhe 79
 Db 311 CTGACCGATTTCTCTGCTCCAGAGTCGACCTCAGCCCTCCCTGGCCATCAGGAGCTC 370
 QY 80 ArgSerGluAlaAspTyrCysAlaAlaTTPaspAspSerLeuSerglyTyr 99
 Db 371 CAGGCTGAGGATAGGCTGATTTATCTGCACTCTATGACAGCAGCTGAGTGTG 430
 QY 100 ValPheGlyGlyGlyThrLeuThrValLeuGly 111
 Db 431 GTATTTCGGCGAGGAGCAAGCTGACCGCTCTCGT 466

RESULT 13
 US-09-240-274-124
 ; Sequence 124, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; FILE REFERENCE: 09596-4202
 ; CURRENT APPLICATION NUMBER: US/09/240,274
 ; EARLIER FILING DATE: 1999-01-29
 ; EARLIER APPLICATION NUMBER: 60/081,380
 ; EARLIER FILING DATE: 1998-04-10
 ; EARLIER APPLICATION NUMBER: 60/028,550
 ; EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 124
 ; LENGTH: 327
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) chain L03
 ; US-09-240-274-124

Alignment Scores:
 Pred. No.: 1.47e-45 Length: 327
 Score: 476.00 Matches: 91
 Percent Similarity: 89.7% Conservative: 5
 Best Local Similarity: 85.0% Mismatches: 11
 Query Match: 81.0% Indels: 0
 DB: 3 Gaps: 0

US-10-092-640-36 (1-111) x US-09-240-274-124 (1-327)

QY 4 LeuThrGlnProProSerValSerAlaAlaProGlyGlnValThrIleSerglySer 23
 Db 7 CTCACACGACCACTCCAGCTGTGGAGCCCGGGGCAAGGATCCATCTTCTTCTTCT 66
 QY 24 GlySerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeuProGlyThr 43
 Db 67 GGCAGAGAGTCCACATCGGAATATATCATGTAGAGTGTATCCAGCACTCCAGAGAAAG 126
 QY 44 AlaProLeuLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValProAspArgPhe 63
 Db 127 GCCCCCAAACTCCTCATCTATCTATATGATGTCAGCGGCGCTCAGGAGGCTCCATTC 186
 QY 64 SerGlySerTyrSerGlyThrSerAlaSerLeuAlaIleSerglyPheArgSerGluAsp 83

```
Db      187 TCTGGCTCCAGTCTGACCTCAGCTCCCTGCGCATCATGAGGCGCTCCAGTCTGAGAT 246
Qy      84 GUAIAASPITYTCYSAIAAATPASPASPSeuSerGlyTyrValPheGlyGly 103
Db      247 GAGGCTGATTATATATGTCAGACATGACAGCCTCATGATCCGGTTCGGCGGA 306
Qy      104 GlyThrLysLeuThrValLeu 110
Db      307 GGGACCAAGCTGACCTCCTC 327

RESULT 14
US-09-848-798-124
; Sequence 124, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIORITY FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain L03
US-09-848-798-124

Alignment Scores:
Pred. No.: 1,47e-45 Length: 327
Score: 476.00 Matches: 91
Percent Similarity: 89.7% Conservative: 5
Best Local Similarity: 85.0% Mismatches: 11
Query Match: 81.0% Indels: 0
Gaps: 0
DB: 3

US-10-092-640-36 (1-111) x US-09-848-798-124 (1-327)
Qy      4 LeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIleSerCysSer 23
Db      7 CTCACCTCAGCCACCTCTCAGCGTCTGGAGACCCCGGGGAGAGGATCACCATCTCTGTTCT 66
Qy      24 GlySerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeuProGlyThr 43
Db      67 GGCAGTAGTCCACACATCGGAATATATCATGTAGAGTGTACACAGCACTCCAGAGAAATG 126
Qy      44 AlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValProAspArgPhe 63
Db      127 GCCCCAAACTCTCATCTATCTAATGTCAGCGGCCCTCAGGGGTCCCTGACCGATTC 186
Qy      64 SerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArgSerGlyuAsp 83
Db      187 TCTGGCTCCAAAGTGGCAGCTCAGCCTCCGCGCATGAGCGGCTCCAGTCTGAGGAT 246
Qy      84 GUAIAASPITYTCYSAIAAATPASPASPSeuSerGlyTyrValPheGlyGly 103
Db      247 GAGGCTGATTATATATGTCAGACATGACAGCCTCATGATCCGGTTCGGCGGA 306
Qy      104 GlyThrLysLeuThrValLeu 110
Db      307 GGGACCAAGCTGACCTCCTC 327

RESULT 15
US-09-372-425A-3
; Sequence 3, Application US/09372425A
; Patent No. 6475749
```

```
; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenakmp, David J.
; REGISTRATION NUMBER: 29,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 nucleotides
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Light chain - DNA
US-09-372-425A-3

Alignment Scores:
Pred. No.: 4,21e-45 Length: 705
Score: 476.00 Matches: 88
Percent Similarity: 88.3% Conservative: 10
Best Local Similarity: 79.3% Mismatches: 13
Query Match: 81.0% Indels: 0
Gaps: 0
DB: 3

US-10-092-640-36 (1-111) x US-09-372-425A-3 (1-705)
Qy      1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
Db      55 CAGTCTGTTTACCGACCGCCCTCAGTGTGCGGCCCAAGAGAGGTCAACATC 114
Qy      21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTyrTyrGlnGlnLeu 40
Db      115 TCTGCTCTCGAAGAGAGCTCCACACTTGGAAATATATATGATCTGTGATACAGCATTC 174
Qy      41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
Db      175 CCAGAAACAGCCCCCAACTTCTCATTTATGACAAATATATCAGCCGCTCAGGGGATTCCT 234
Qy      61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      235 GACCGATTCTCGGCTCCAAAGTGGCAGCTGACGACCCCTGGGCATCACGGACTCCAG 294
Qy      81 SerGluAspGluAlaAspTyrTyrCysAlaAlaATPASPASPSeuSerLysSerGlyTyrVal 100
Db      295 ACTGGGAGAGAGACCGATTATTAATCGGGAACATGAGATGACGCTGATGCTGAGCTT 354
Qy      101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db      355 TTCCGGCGAGAGGAGCGAAGTAGACCTCTCTAGGT 387
```

Fri May 26 08:42:23 2006

us-10-092-640-36.rni

Page 9

Search completed: May 25, 2006, 20:50:31
Job time : 147.3 secs

This Page Blank (uspro)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 20:50:52 ; Search time 1008.71 Seconds
(without alignments)
2028.220 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588

Sequence: 1 GSVLTQPPPSVAAPGOKVTI.....WDSLSGWVFGGSTRKTLVIG 111

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+pn.model -DEV=xlh
-O=/abs/ABSSWB.epool/US10092640/runat_25052006.155727.6087/app.query.fasta_1
-DB=Published Applications NA.Main -OPMT=fastap -SUFFIX=rnphm -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -POCALIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pico -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs602h
-USER=US10092640 @CEN 1.1 2332 @runat_25052006.155727.6087 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main:*

1:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
5:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
6:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588	100.0	765	3	US-09-888-721-35 Sequence 35, Appl

2	566	96.3	807	3	US-09-888-721-37	Sequence 37, Appl
3	566	96.3	806	3	US-09-888-721-39	Sequence 39, Appl
4	566	96.3	801	3	US-09-888-721-41	Sequence 41, Appl
5	566	96.3	873	3	US-09-888-721-45	Sequence 45, Appl
6	566	96.3	888	3	US-09-888-721-43	Sequence 43, Appl
7	553	94.0	333	9	US-10-679-032-36	Sequence 36, Appl
8	545	92.7	333	9	US-10-679-032-6	Sequence 6, Appl
9	536	91.2	333	9	US-10-679-032-30	Sequence 30, Appl
10	533.5	90.7	336	9	US-10-679-032-2	Sequence 2, Appl
11	531	90.3	333	9	US-10-679-032-34	Sequence 34, Appl
12	529	90.0	333	9	US-10-679-032-38	Sequence 38, Appl
13	527	89.6	333	9	US-10-679-032-12	Sequence 12, Appl
14	525	89.3	333	9	US-10-679-032-18	Sequence 18, Appl
15	524.5	89.2	336	9	US-10-679-032-20	Sequence 20, Appl
16	521	88.6	333	9	US-10-679-032-28	Sequence 28, Appl
17	520	88.4	333	9	US-10-679-032-22	Sequence 22, Appl
18	517	87.9	732	8	US-10-779-461-87	Sequence 87, Appl
19	516	87.8	333	9	US-10-679-032-12	Sequence 12, Appl
20	516	87.8	744	9	US-10-800-023-18	Sequence 18, Appl
21	516	87.8	908	8	US-10-375-356A-9	Sequence 9, Appl
22	513	87.2	2635	6	US-10-198-846-13529	Sequence 13529, A
23	511	86.9	411	9	US-10-783-411-27	Sequence 27, Appl
24	510	86.7	333	9	US-10-679-032-24	Sequence 24, Appl
25	510	86.7	354	10	US-10-916-6758-28	Sequence 28, Appl
26	510	86.7	762	13	US-10-916-847-214	Sequence 214, Appl
27	508	86.4	327	3	US-09-848-798-128	Sequence 128, Appl
28	508	86.4	327	15	US-11-064-174-128	Sequence 128, Appl
29	507	86.2	328	9	US-10-679-032-26	Sequence 26, Appl
30	504	85.7	333	9	US-10-844-424-7	Sequence 7, Appl
31	503	85.5	768	3	US-09-747-669-4	Sequence 4, Appl
32	503	85.5	768	3	US-09-747-669-5	Sequence 5, Appl
33	503	85.5	768	6	US-10-290-703-4	Sequence 4, Appl
34	503	85.5	768	6	US-10-290-703-5	Sequence 5, Appl
35	502.5	85.5	441	3	US-09-988-115A-56	Sequence 56, Appl
36	502.5	85.5	441	10	US-10-705-519-56	Sequence 56, Appl
37	501	85.2	366	11	US-10-993-543-45	Sequence 45, Appl
38	500	85.0	333	9	US-10-679-032-32	Sequence 32, Appl
39	500	85.0	1640	6	US-10-198-846-13206	Sequence 13206, A
40	499	84.9	735	10	US-10-935-290-215	Sequence 215, Appl
41	499	84.9	780	10	US-10-935-290-213	Sequence 213, Appl
42	498	84.7	1565	6	US-10-198-846-13276	Sequence 13276, A
43	496	84.4	870	10	US-10-276-233A-4	Sequence 4, Appl
44	495	84.2	330	10	US-10-727-145-211	Sequence 211, Appl
45	495	84.2	366	11	US-10-993-543-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-888-721-35
Sequence 35, Application US/09888721
Patent No. US20020132990A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Wile, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Scheman, Daniel
TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 765
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Human/murine
OTHER INFORMATION: chimeric single chain binding polypeptide (C6.5
OTHER INFORMATION: sfv)
US-09-888-721-35

Alignment Scores:

Pred. No.:	8,19e-65	Length:	765
Score:	588.00	Matches:	111
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-092-640-36 (1-111) x US-09-888-721-35 (1-765)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 433 CAGTCTGTGTGACGAGCGCGCCCTCAGTGTGCGGCCCCAGGACAGAGGTCAACCATC 492
QY 21 SerCysSerGlySerSerSerSerAniIegIyaSnaSnyrValSerTrpTyrgIngnIleu 40
DB 493 TCTGCTCTGGAAGCAGCTCCACATTTGGAAATATATATATCTGTGTACCAAGCAGCTC 552
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgIyHsThrAsnArgProAlaGlyValPro 60
DB 553 CCAGGAACAGCCCCCAAACTCCTCATCTATGTGTACACCAATGCGCCGAGGGGTCCT 612
QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 613 GACCGATTCTCGGCTCCCAAGTCTGACCTCAGCTCCCTGCGCCATCAGTGGTCCGG 672
QY 81 SerGluAspGluAlaAspTyrrTyrcysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100
DB 673 TCCGAGATGAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 732
QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
DB 733 TTCGGCGAGGAGCAAGCTGACCGTCTTAGGT 765

RESULT 2

US-09-888-721-37
Sequence 37, Application US/09888721
Patent No. US20020132990A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Sherman, Daniel
TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 807
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Human/murine
OTHER INFORMATION: chimeric single chain binding polypeptide (C6ML3-9
OTHER INFORMATION: sfv/)
US-09-888-721-37

Alignment Scores:

Pred. No.:	5,72e-62	Length:	807
Score:	566.00	Matches:	107
Percent Similarity:	98.2%	Conservative:	2

Best Local Similarity:	96.4%	Mismatches:	2
Query Match:	96.3%	Indels:	0
DB:	3	Gaps:	0

US-10-092-640-36 (1-111) x US-09-888-721-37 (1-807)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 433 CAGTCTGTGTGACGAGCGCGCCCTCAGTGTGCGGCCCCAGGACAGAGGTCAACCATC 492
QY 21 SerCysSerGlySerSerSerSerAniIegIyaSnaSnyrValSerTrpTyrgIngnIleu 40
DB 493 TCTGCTCTGGAAGCAGCTCCACATTTGGAAATATATATATCTGTGTACCAAGCAGCTC 552
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgIyHsThrAsnArgProAlaGlyValPro 60
DB 553 CCAGGAACAGCCCCCAAACTCCTCATCTATGTGTACACCAATGCGCCGAGGGGTCCT 612
QY 61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
DB 613 GACCGATTCTCGGCTCCCAAGTCTGACCTCAGCTCCCTGCGCCATCAGTGGTCCGG 672
QY 81 SerGluAspGluAlaAspTyrrTyrcysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 100
DB 673 TCCGAGATGAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 732
QY 101 PheGlyGlyGlyThrIysLeuThrValLeuGly 111
DB 733 TTCGGCGAGGAGCAAGCTGACCGTCTTAGGT 765

RESULT 3

US-09-888-721-39
Sequence 39, Application US/09888721
Patent No. US20020132990A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Marasco, Wayne A.
APPLICANT: Sherman, Daniel
TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 846
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Human/murine
OTHER INFORMATION: chimeric single chain binding polypeptide
OTHER INFORMATION: (C6ML-3-9sfv-L1-KDEL)
US-09-888-721-39

Alignment Scores:

Pred. No.:	6,07e-62	Length:	846
Score:	566.00	Matches:	107
Percent Similarity:	98.2%	Conservative:	2
Best Local Similarity:	96.4%	Mismatches:	2
Query Match:	96.3%	Indels:	0
DB:	3	Gaps:	0

US-10-092-640-36 (1-111) x US-09-888-721-39 (1-846)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
DB 433 CAGTCTGTGTGACGAGCGCGCCCTCAGTGTGCGGCCCCAGGACAGAGGTCAACCATC 492


```

Db      733 TTGGGGGAGGAACCAAGCTGACCGTCTAGGT 765
|||||
RESULT 6
US-09-888-721-43
; Sequence 43, Application US/09888721
; Patent No. US2002013290A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scheetman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6ML3-9sFv'-L2-H14)
US-09-888-721-43

Alignment Scores:
Pred. No.:      6,45e-62      Length:      888
Score:          566.00      Matches:     107
Percent Similarity: 98.2%      Conservative: 2
Best Local Similarity: 96.4%      Mismatches:  2
Query Match:    96.3%      Indels:      0
Db:              3          Gaps:              0

US-10-092-640-36 (1-111) x US-09-888-721-43 (1-888)
QY      1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIysValThrIle 20
      |||
Db      433 CAGTCTGTGTACCGACGCGCCCTCAGTCTGCGGCCCGACGAGCAAGGTCACCATC 492
QY      21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTrpValSerTrpTyrGlnGlnIleu 40
      |||
Db      493 TCCTGCTCTGGAAGCAGCTCCAAACATGGGAATTAATTATGATCTCGTACCGACGAGCTC 552
QY      41 ProGlyThrAlaProIlyIleuIleuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
      |||
Db      553 CCAGGAACAGCCCCCAACTCCTCATCTATGATCAACCAATCGGCCCGACAGGGGTCCCT 612
QY      61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerIleAlaIleSerGlyPheArg 80
      |||
Db      613 GACCGATTCTCTGGCTCCAGTCTGGACCTCAGCTCCCTGGCATTCAGTGGTTCCGG 672
QY      81 SerGluAspGluAlaAspTyrTrpCysAlaAlaATPAspAspSerIleuSerGlyTrpVal 100
      |||
Db      673 TCCGAGGATGAGGCTGATTATTACTGTGCTCCTGGGACTACACCCCTCGGGGCTGGGTG 732
QY      101 PheGlyGlyGlyThrIlyIleuThrValIleuGly 111
      |||
Db      733 TTGGGGGAGGAACCAAGCTGACCGTCTAGGT 765

```

```

; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; TITLE OF INVENTION: TREATMENT OF ATHEROSCLEROSIS
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 36
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-36

Alignment Scores:
Pred. No.:      8,69e-61      Length:      333
Score:          553.00      Matches:     103
Percent Similarity: 96.4%      Conservative: 4
Best Local Similarity: 92.8%      Mismatches:  4
Query Match:    94.0%      Indels:      0
Db:              9          Gaps:              0

US-10-092-640-36 (1-111) x US-10-679-032-36 (1-333)
QY      1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIysValThrIle 20
      |||
Db      1 CAGTCTGTGTACCTACGACCACTCAGGCTGTGGAGCCCGGGGACAGGCTCACCATC 60
QY      21 SerCysSerGlySerSerSerAsnIleGlyAsnAsnTrpValSerTrpTyrGlnGlnIleu 40
      |||
Db      61 TCCTGCTCTGGAAGCAGCTCCAAACATGGGAATTAATTATGATCTCGTACCGACGAGCTC 120
QY      41 ProGlyThrAlaProIlyIleuIleuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
      |||
Db      121 CCAGGAACGCCCCCAACTCCTCATCTATGATCAACCAATCGGCCCGACAGGGGTCCCT 180
QY      61 AspArgPheSerGlySerIysSerGlyThrSerAlaSerIleAlaIleSerGlyPheArg 80
      |||
Db      181 GACCGATTCTCTGGCTCCAGTCTGGACCTCAGCTCCCTGGCATTCAGTGGCTCCGG 240
QY      81 SerGluAspGluAlaAspTyrTrpCysAlaAlaATPAspAspSerIleuSerGlyTrpVal 100
      |||
Db      241 TCCGAGGATGAGGCTGATTATTACTGTGCTCAGCATGAGATGACAGTCTGAGTGGGTG 300
QY      101 PheGlyGlyGlyThrIlyIleuThrValIleuGly 111
      |||
Db      301 TTGGGGGAGGAACCAAGCTGACCGTCTAGGT 333

```

```

RESULT 7
US-10-679-032-36
; Sequence 36, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-6

Alignment Scores:
Pred. No.: 9,18e-60 Length: 333
Score: 545.00 Matches: 102
Percent Similarity: 95.5% Conservative: 4
Best Local Similarity: 91.9% Mismatches: 5
Query Match: 92.7% Indels: 0
DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x US-10-679-032-6 (1-333)

QY 1 GlnSerValLeuThrGlnProPserValSerAlaAlaProGlyGlnLysValThrIle 20
Db 1 CAGTCTGTGCTGACTCAGCCACCCTCAGGCTGGGACCCCGGCGAGAGGTCACATC 60
QY 21 SerCysSerGlySerSerSerAenIleGlyAsnAsnTyValSerTPYrGlnGlnLeu 40
Db 61 TCTGTCTCGAAGAGCTCCATATCGGAAGTAATTATGTATCTCGGTATCAGCAGCTC 120
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
Db 121 CAGGAAACGGCCCCCAAACTCTCATCTATGTGTAACATCAGCATCGGCCCTCAGGGGTCCCT 180
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db 181 GACCGATTCTCTGGCTCCAAAGTCTGGCACTCAGCCTCCCTGGCCATCAGTGGGCTCCCG 240
QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTTPAspAspSerLeuSerGlyTPVal 100
Db 241 TCCGAGATGAGGCTGATTAATTACTGTGACGATGAGATGACACGCTGAGTGGTG 300
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 301 TTCGGCGAGGAAACCAAGCTGACGGTCTTAGGT 333

RESULT 9
US-10-679-032-30
; Sequence 30, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; TITLE OF INVENTION: TREATMENT OF ATHEROSCLEROSIS
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 30
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-30

Alignment Scores:
Pred. No.: 1,3e-58 Length: 333
Score: 536.00 Matches: 100
Percent Similarity: 94.6% Conservative: 5
Best Local Similarity: 90.1% Mismatches: 6
Query Match: 91.2% Indels: 0
DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x US-10-679-032-30 (1-333)

```

```

QY 1 GlnSerValLeuThrGlnProPserValSerAlaAlaProGlyGlnLysValThrIle 20
Db 1 CAGTCTGTGCTGACTCAGCCACCCTCAGGCTGGGACCCCGGCGAGAGGTCACATC 60
QY 21 SerCysSerGlySerSerSerAenIleGlyAsnAsnTyValSerTPYrGlnGlnLeu 40
Db 61 TCTGTCTCGAAGAGCTCCATATCGGAAGTAATTATGTATCTCGGTATCAGCAGCTC 120
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
Db 121 CAGGAAACGGCCCCCAAACTCTCATCTATGTGTAACATCAGCATCGGCCCTCAGGGGTCCCT 180
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db 181 GACCGATTCTCTGGCTCCAAAGTCTGGCACTCAGCCTCCCTGGCCATCAGTGGGCTCCCG 240
QY 81 SerGluAspGluAlaAspTyTyTyCysAlaAlaTTPAspAspSerLeuSerGlyTPVal 100
Db 241 TCCGAGATGAGGCTGATTAATTACTGTGACGATGAGATGACACGCTGAGTGGTG 300
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 301 TTCGGCGAGGAAACCAAGCTGACGGTCTTAGGT 333

RESULT 10
US-10-679-032-2
; Sequence 2, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; TITLE OF INVENTION: TREATMENT OF ATHEROSCLEROSIS
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-2

Alignment Scores:
Pred. No.: 2,75e-58 Length: 336
Score: 533.50 Matches: 101
Percent Similarity: 93.8% Conservative: 4
Best Local Similarity: 90.2% Mismatches: 6
Query Match: 90.7% Indels: 1
DB: 9 Gaps: 1

US-10-092-640-36 (1-111) x US-10-679-032-2 (1-336)

QY 1 GlnSerValLeuThrGlnProPserValSerAlaAlaProGlyGlnLysValThrIle 20
Db 1 CAGTCTGTGCTGACTCAGCCACCCTCAGGCTGGGACCCCGGCGAGAGGTCACATC 60
QY 21 SerCysSerGlySerSerSerAenIleGlyAsnAsnTyValSerTPYrGlnGlnLeu 40
Db 61 TCTGTCTCGAAGAGCTCCAAAGTCTGGCACTCAGCCTCCCTGGCCATCAGTGGGCTCCCG 120
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrgLysIleThrAsnArgProAlaGlyValPro 60
Db 121 CAGGAAACGGCCCCCAAACTCTCATCTATGTGTAACATCAGCATCGGCCCTCAGGGGTCCCT 180
QY 61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80

```

```
Db      181 GACCATTCCTCGGCTCCAAAGTCTGGACCTCAGCCTCCCTGCGCATCGTGGGCTCCGG 240
        |||
Qy      81 SerGluaspGluAlaaspTyrTyrCysAlaAlaATPaspaspSerleuSerGly--Tyr 99
        |||
Db      241 TCCGAGGATGAGGCTGATTAATTACTGTGAGCATGGATGACAGCTGTAATGTCATTGG 300
        |||
Qy      100 ValPheGlyGlyThrlYsleuThrValleuGly 111
        |||
Db      301 GTTTCGGGGGAGGAACCAAGCTGACGGTCTTAGGT 336

RESULT 11
US-10-679-032-34
; Sequence 34, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-34

Alignment Scores:
Pred. No.:      5,68e-58      Length:      333
Score:          531.00      Matches:      99
Percent Similarity: 93.7%      Conservative: 5
Best Local Similarity: 89.2%      Mismatches: 7
Query Match:    90.3%      Indels:      0
DB:             9          Gaps:      0

US-10-092-640-36 (1-111) x US-10-679-032-34 (1-333)

Qy      1 GlnSerValleuThrGlnProSerValSerAlaAlaProGlyGlnYsValThrIle 20
        |||
Db      1 CAGTCTGTCTGACTCAGCCACCTCAGGGCTCGGGACCCCGGGGAGAGGGTCAACCATC 60
        |||
Qy      21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
        |||
Db      61 TCCTTCTTCGAGAGAGAGCTCAACATCGGAATAATGTAACGTAATCAGACAGCTC 120
        |||
Qy      41 ProGlyThrAlaProlysleuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
        |||
Db      121 CCAGAGACGGCCCCCAAACTCCTCATCTATGTGTACACAAATCGGCGCTCAGGGGTCCCT 180
        |||
Qy      61 AspArgPheSerGlySerIleSerSerGlyThrSerAlaSerleuAlaIleSerGlyPheArg 80
        |||
Db      181 GACCATTCCTCGGCTCCAAAGTCTGGACCTCAGCCTCCCTGCGCATCGTGGGCTCCGG 240
        |||
Qy      81 SerGluaspGluAlaaspTyrTyrCysAlaAlaATPaspaspSerleuSerGlyTyrPVal 100
        |||
Db      241 TCCGAGGATGAGGCTGATTAATTACTGTGAGCATGGATGACAGCTGCGTGGTGGCTGG 300
        |||
Qy      101 PheGlyGlyGlyThrlYsleuThrValleuGly 111
        |||
Db      301 TTCGGCGGAGGAACCAAGCTGACGGTCTTAGGT 333

RESULT 12
US-10-679-032-8
; Sequence 8, Application US/10679032
```

```
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-8

Alignment Scores:
Pred. No.:      1.02e-57      Length:      333
Score:          529.00      Matches:      99
Percent Similarity: 92.8%      Conservative: 4
Best Local Similarity: 89.2%      Mismatches: 8
Query Match:    90.0%      Indels:      0
DB:             9          Gaps:      0

US-10-092-640-36 (1-111) x US-10-679-032-8 (1-333)

Qy      1 GlnSerValleuThrGlnProSerValSerAlaAlaProGlyGlnYsValThrIle 20
        |||
Db      1 CAGTCTGTCTGACTCAGCCACCTCAGGGCTCGGGACCCCGGGGAGAGGGTCAACCATC 60
        |||
Qy      21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
        |||
Db      61 TCCTTCTTCGAGAGAGAGCTCAACATCGGAATAATGTAACGTAATCAGACAGCTC 120
        |||
Qy      41 ProGlyThrAlaProlysleuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
        |||
Db      121 CCAGAGACGGCCCCCAAACTCCTCATCTATGTGTACAAATCGGCGCTCAGGGGTCCCT 180
        |||
Qy      61 AspArgPheSerGlySerIleSerSerGlyThrSerAlaSerleuAlaIleSerGlyPheArg 80
        |||
Db      181 GACCATTCCTCGGCTCCAAAGTCTGGACCTCAGCCTCCCTGCGCATCGTGGGCTCCGG 240
        |||
Qy      81 SerGluaspGluAlaaspTyrTyrCysAlaAlaATPaspaspSerleuSerGlyTyrPVal 100
        |||
Db      241 TCCGAGGATGAGGCTGATTAATTACTGTGAGCATGGATGACAGCTGAGTCAATTGGCTGG 300
        |||
Qy      101 PheGlyGlyGlyThrlYsleuThrValleuGly 111
        |||
Db      301 TTCGGCGGAGGAACCAAGCTGACGGTCTTAGGT 333

RESULT 13
US-10-679-032-38
; Sequence 38, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679,032
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 38
```

```

; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-38

```

```

Alignment Scores:
Pred. No.: 1.84e-57 Length: 333
Score: 527.00 Matches: 98
Percent Similarity: 93.7% Conservative: 6
Best Local Similarity: 88.3% Mismatches: 7
Query Match: 89.6% Indels: 0
DB: 9 Gaps: 0

```

US-10-092-640-36 (1-111) x US-10-679-032-38 (1-333)

```

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
Db 1 CAGTCTGTGCTGACTGACCCACCTCAGCCTGCGGACCCCGGAGAGGTCACCATC 60
   |||||
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
   |||||
Db 61 TCCTGCTCTGGAGAGCAGCTCAGCATTGGGAATTAATTATCTGTTATCTGATCAGCAGCTC 120
   |||||
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
   |||||
Db 121 CCAGGAACGGCCCCCAAACTCCTCATCTATGACAAATATTAAGGAGACCTCAGGAGGTCCTT 180
   |||||
QY 61 AspArgPheSerGlySerGlySerGlySerGlySerSerAlaSerLeuAlaIleSerGlyPheArg 80
   |||||
Db 181 GACCATTCCTGCTGCTCCTCAAGTCTGACCTGACCTCCTGCGCATCAGTGGGCTCCGG 240
   |||||
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTyrAspAspSerLeuSerGlyTyrPval 100
   |||||
Db 241 TCCGAGATGAGGCTGATTATTAATCTGTCGACATGGGATGACAGCTGAATGTTGGGTG 300
   |||||
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
   |||||
Db 301 TTCGGCGGAGGAACCAAGCTGACGCTTAGGT 333

```

RESULT 14

```

US-10-679-032-10
; Sequence 10, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679, 032
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-10

```

```

Alignment Scores:
Pred. No.: 3.32e-57 Length: 333
Score: 525.00 Matches: 98
Percent Similarity: 91.9% Conservative: 4
Best Local Similarity: 88.3% Mismatches: 9
Query Match: 89.3% Indels: 0

```

DB: 9 Gaps: 0

US-10-092-640-36 (1-111) x US-10-679-032-10 (1-333)

```

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
Db 1 CAGTCTGTGCTGACTGACCCACCTCAGCCTTGGGACCCCGGAGAGGTCACCATC 60
   |||||
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
   |||||
Db 61 TCCTGCTCTGGAGAGCAGCTCCAACATTGGGAATTAATTATCTGTTATCTGATCAGCAGCTC 120
   |||||
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
   |||||
Db 121 CCAGGAACGGCCCCCAAACTCCTCATCTATGAGAAATATTCAGGAGGTCCTT 180
   |||||
QY 61 AspArgPheSerGlySerGlySerGlySerGlySerSerAlaSerLeuAlaIleSerGlyPheArg 80
   |||||
Db 181 GACCATTCCTGCTGCTCCTCAAGTCTGACCTTAGCTCCTGCGCATCAGTGGGCTCCGG 240
   |||||
QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaIleTyrAspAspSerLeuSerGlyTyrPval 100
   |||||
Db 241 TCCGAGATGAGGCTGATTATTAATCTGTCGACATGGGATGACAGCTGAATGTTGGGTG 300
   |||||
QY 101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
   |||||
Db 301 TTCGGCGGAGGAACCAAGCTGACGCTTAGGT 333

```

RESULT 15

```

US-10-679-032-20
; Sequence 20, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
; FILE REFERENCE: 7303CIP
; CURRENT APPLICATION NUMBER: US/10/679, 032
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-10-679-032-20

```

```

Alignment Scores:
Pred. No.: 3.9e-57 Length: 336
Score: 524.50 Matches: 100
Percent Similarity: 92.9% Conservative: 4
Best Local Similarity: 89.3% Mismatches: 7
Query Match: 89.2% Indels: 1
DB: 9 Gaps: 1

```

US-10-092-640-36 (1-111) x US-10-679-032-20 (1-336)

```

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
Db 1 CAGTCTGTGCTGACTGACCCACCTCAGCCTTGGGACCCCGGAGAGGTCACCATC 60
   |||||
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 40
   |||||
Db 61 TCCTGCTCTGGAGAGCAGCTCCAACATTGGGAATTAATTATCTGTTATCTGATCAGCAGCTC 120
   |||||
QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
   |||||

```

```

Db      121  CCAGGACGGCCCCCAACTCTCATCTATAGGAATATCAGGGCCCTCAGGGGTCCCT 180
QY      61  AsparGpneSerGlySerIySerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
Db      181  GACCGATTCTCTGGGCTCCAAAGCTGGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
QY      81  SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGly---Trp 99
Db      241  TCCGAGGATGAGGCTGATTATTACTGTGCAAGCATGGGATGACAGCCTGAAATGTCATTGG 300
QY      100 ValPheGlyGlyThrIyLeuThrValLeuGly 111
Db      301  GTGTTGGGGGAGGAACCAAGCTGAAGGTCTAGGT 336
  
```

Search completed: May 25, 2006, 21:27:49
 Job time : 1011.71 secs

us-10-092-640-36.rnpbm

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 20:51:32 ; Search time 17.575 Seconds

(without alignments)
1069.431 Million cell updates/sec

Title: US-10-092-640-36

Perfect score: 588
Sequence: 1 QSVLTNPSPVSAAPGQKVTI.....WDSLSGWVFGGSKLTIVLG 111

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ .p2n.model -DEV=xlh
-Q=/abs/ABSSMBE.spool/US10092640/runat_25052006_155730_6141/app.query.fasta_1
-DB=Published Applications NA New -OPMT=fastcap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-PPANS=human0.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss02h
-USER=US10092640 @CGN 1 1 26 @runat_25052006_155730_6141 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORES=0 -WAIT -DSELOCK=100 -LONGLOG -DEV TIMEOUT=10
-NARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:
1: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505.5	86.0	764	6	US-10-503-433B-11 Sequence 11, Appl
2	497.5	84.6	732	6	US-10-503-433B-11 Sequence 16, Appl
3	497.5	84.6	795	6	US-10-503-433B-12 Sequence 12, Appl
4	493.5	83.9	873	7	US-11-154-103-27 Sequence 27, Appl
5	493.5	83.9	873	7	US-11-154-103-28 Sequence 28, Appl
6	490.5	82.4	801	6	US-10-503-433B-14 Sequence 14, Appl
7	484.5	83.4	796	6	US-10-503-433B-24 Sequence 24, Appl
8	466.5	79.3	803	6	US-10-503-433B-20 Sequence 20, Appl
9	456.5	77.6	792	6	US-10-503-433B-21 Sequence 21, Appl

10	454.5	77.3	779	6	US-10-503-433B-18	Sequence 18, Appl
11	452	76.9	333	7	US-11-254-679-31	Sequence 31, Appl
12	451.5	76.8	722	6	US-10-503-433B-22	Sequence 22, Appl
13	444.5	75.6	706	6	US-10-503-433B-17	Sequence 17, Appl
14	436.5	73.8	704	6	US-10-503-433B-15	Sequence 15, Appl
15	434	73.2	864	7	US-11-154-103-29	Sequence 29, Appl
16	431.5	73.4	330	7	US-11-254-679-63	Sequence 63, Appl
17	424.5	72.2	707	6	US-10-503-433B-19	Sequence 19, Appl
18	420	71.4	1954	7	US-11-293-697-1648	Sequence 1648, Ap
19	412	70.1	1912	7	US-11-293-697-1818	Sequence 1818, Ap
20	409	69.6	885	7	US-11-154-103-33	Sequence 33, Appl
21	399	67.9	330	6	US-10-499-666-13	Sequence 13, Appl
22	392	66.7	729	7	US-11-154-103-20	Sequence 20, Appl
23	385.5	65.6	870	7	US-11-154-103-30	Sequence 30, Appl
24	356	60.5	873	7	US-11-154-103-32	Sequence 32, Appl
25	335.5	57.1	637	6	US-10-503-433B-23	Sequence 23, Appl
26	334	56.8	2081	7	US-11-293-697-2348	Sequence 2348, Ap
27	333	56.6	330	7	US-11-300-563-24	Sequence 24, Appl
28	332	56.5	543	7	US-11-301-554-970	Sequence 970, Appl
29	317	53.9	4027	7	US-11-169-140-1	Sequence 1, Appl
30	298	50.7	608	7	US-11-301-554-908	Sequence 908, Appl
31	284	48.3	726	7	US-11-183-125-19	Sequence 19, Appl
32	276.5	47.0	592	6	US-10-503-433B-13	Sequence 13, Appl
33	268	45.6	330	7	US-11-254-679-35	Sequence 35, Appl
34	268	45.6	384	7	US-11-183-218-59	Sequence 59, Appl
35	268	45.6	9209	7	US-11-183-218-58	Sequence 58, Appl
36	267.5	45.5	321	7	US-11-219-563-52	Sequence 52, Appl
37	264.5	45.0	322	7	US-11-211-917-83	Sequence 83, Appl
38	264.5	45.0	705	7	US-11-211-917-87	Sequence 87, Appl
39	262	44.6	333	7	US-11-216-033-11	Sequence 11, Appl
40	261	44.4	384	7	US-11-315-067-3	Sequence 3, Appl
41	261	44.4	384	7	US-11-315-067-5	Sequence 5, Appl
42	260.5	44.3	620	7	US-11-219-563-56	Sequence 56, Appl
43	260.5	44.3	620	7	US-11-219-563-58	Sequence 58, Appl
44	260.5	44.3	2196	7	US-11-155-444-5	Sequence 5, Appl
45	260.5	44.3	2208	7	US-11-155-444-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-503-433B-11
; Sequence 11, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 11
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P8 scFv binding site (template DNA)
US-10-503-433B-11

Alignment Scores:
Pred. No.: 1,53e-47
Score: 505.50
Percent Similarity: 91.1%
Best Local Similarity: 87.5%
Query Match: 86.0%
DB: 6
Length: 764
Matches: 98
Conservative: 9
Mismatch: 9
Indels: 1
Gaps: 1
US-10-092-640-36 (1-111) x US-10-503-433B-11 (1-764)


```

; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-27

Alignment Scores:
Pred. No.: 3,86e-46 Length: 873
Score: 493.50 Matches: 94
Percent Similarity: 92.0% Conservative: 9
Best Local Similarity: 83.9% Mismatches: 8
Query Match: 83.9% Indels: 1
DB: 7 Gaps: 1

US-10-092-640-36 (1-111) x US-11-154-103-27 (1-873)

QY 1 GlnSerValIleuThrgInpProSerValSerAlaAlaProGlyGlnuysValThrIle 20
DB 469 CAGTCTGTGTAGCGAGCGCCCTCAGTGTCTGGGGCCCCAGGAGAGGTCACCATC 528
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 39
DB 529 TCCTGCACGTGGAGGAGCTCCAAACATCGGGGAGGAGTTATGTTACACTGTGTACAGAG 588
QY 40 LeuProGlyThrAlaProIleuLeuIleTyrgIleHisThrAsnArgProAlaGlyVal 59
DB 589 CTTCAGAGAACAGCCCCAAACCTCCATCTATGTGAACCAACATCGGCCCTCAGGGGTC 648
QY 60 ProAspArgPheSerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGly 79
DB 649 CCTGACCGATTCCTGGCTTCAAGTGTGACACTGACCTCCTGCGCATCACTGGGCTC 708
QY 80 ArgSerGluAspGluAlaAspTyTyTyCyAlaAlaIleTyrAspAspSerLeuSerGlyTyr 99
DB 709 CAGGCTGAGAGATGAGGCTGATTATTAATCTCCAGTCTCTATGACAGCAGCTGAGTGGTGG 768
QY 100 ValPheGlyGlyGlyThrylsleuThrValIleuGly 111
DB 769 GTGTTGGCGGAGGAGCAAGCTGACCTGATCTAGGT 804

RESULT 5
US-11-154-103-28
; Sequence 28, Application US/11/154,103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000420US
; CURRENT APPLICATION NUMBER: US/11/154,103
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
```

```

; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-28

Alignment Scores:
Pred. No.: 3,86e-46 Length: 873
Score: 493.50 Matches: 94
Percent Similarity: 92.0% Conservative: 9
Best Local Similarity: 83.9% Mismatches: 8
Query Match: 83.9% Indels: 1
DB: 7 Gaps: 1

US-10-092-640-36 (1-111) x US-11-154-103-28 (1-873)

QY 1 GlnSerValIleuThrgInpProSerValSerAlaAlaProGlyGlnuysValThrIle 20
DB 469 CAGTCTGTGTAGCGAGCGCCCTCAGTGTCTGGGGCCCCAGGAGAGGTCACCATC 528
QY 21 SerCysSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 39
DB 529 TCCTGCACGTGGAGGAGCTCCAAACATCGGGGAGGAGTTATGTTACACTGTGTACAGAG 588
QY 40 LeuProGlyThrAlaProIleuLeuIleTyrgIleHisThrAsnArgProAlaGlyVal 59
DB 589 CTTCAGAGAACAGCCCCAAACCTCCATCTATGTGAACCAACATCGGCCCTCAGGGGTC 648
QY 60 ProAspArgPheSerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGly 79
DB 649 CCTGACCGATTCCTGGCTTCAAGTGTGACACTGACCTCCTGCGCATCACTGGGCTC 708
QY 80 ArgSerGluAspGluAlaAspTyTyTyCyAlaAlaIleTyrAspAspSerLeuSerGlyTyr 99
DB 709 CAGGCTGAGAGATGAGGCTGATTATTAATCTCCAGTCTCTATGACAGCAGCTGAGTGGTGG 768
QY 100 ValPheGlyGlyGlyThrylsleuThrValIleuGly 111
DB 769 GTGTTGGCGGAGGAGCAAGCTGACCTGATCTAGGT 804

RESULT 6
US-10-503-433B-14
; Sequence 14, Application US/10/503,433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 14
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-9
US-10-503-433B-14

Alignment Scores:
Pred. No.: 7,41e-46 Length: 801
Score: 490.50 Matches: 96
```

Percent Similarity: 90.2% Conservative: 5
Best Local Similarity: 85.7% Mismatches: 10
Query Match: 83.4% Indels: 1
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-14 (1-801)

```
OY 1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
   |||
Db 397 CAGTCTGTGCTACTCAGCCACCTCAGGCTCTGGAGACCCCGGAGAGGGTCAACATC 456
OY 21 SerCySerGlySerSerSerSerAniIleGlyAsnAsnTyR---ValSerTrpYrGlnGln 39
   |||
Db 457 TCTTGCACTGGAGAGAGCTCCCAACATCGGGGAGGTTAGATGATACATCGATATCAGCAG 516
OY 40 LeuProGlyThrAlaProIlySerLeuLeuIleTyRgIlyHisThrAsnArgProAlaGlyVal 59
   |||
Db 517 CTCCGAGGAAACGGCCCAACTCCTCATCTATGTGTACAAACATCGGCCCTCAGGGGCTC 576
OY 60 ProAspArgPheSerGlySerIlySerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
   |||
Db 577 CTGACCGATTTCTTGCTCCAAAGTGGACCTCAGCTTCCCTGCGCATCAGTGGGCTC 636
OY 80 ArgSerGluAspGluAlaAspTyRyCySaIaAlaIleTrpAspAspSerLeuSerGlyTrp 99
   |||
Db 637 CGGTCGAGAGATGAGGCTGATTATTACTGTGCGGCTCATGATGACAGTATCAGCGGTTG 696
OY 100 ValPheGlyGlyGlyThrIlySerLeuThrValLeuGly 111
   |||
Db 697 GTGTTGCGGAGAGAACCAAGCTGAGCGGTCTAGGT 732
```

RESULT 7

US-10-503-433B-24

```
; Sequence 24, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 24
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-18
US-10-503-433B-24
```

Alignment Scores:

Pred. No.:	3,39e-45	Length:	796
Score:	484.50	Matches:	94
Percent Similarity:	90.2%	Conservative:	7
Best Local Similarity:	83.9%	Mismatches:	10
Query Match:	82.4%	Indels:	1
DB:	6	Gaps:	1

US-10-092-640-36 (1-111) x US-10-503-433B-24 (1-796)

```
OY 1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
   |||
Db 397 CAGTCTGTGCTACTCAGCCACCTCAGGCTCTGGAGACCCCGGAGAGGGTCAACATC 456
OY 21 SerCySerGlySerSerSerSerAniIleGlyAsnAsnTyR---ValSerTrpYrGlnGln 39
   |||
Db 457 TCTTGCACTGGAGAGAGCTCCCAACATCGGGGAGGTTAGATGATACATCGATATCAGCAG 516
```

```
OY 40 LeuProGlyThrAlaProIlySerLeuLeuIleTyRgIlyHisThrAsnArgProAlaGlyVal 59
   |||
Db 517 CTCCGAGGAAACGGCCCAACTCCTCATCTATGTGTACAAACATCGGCCCTCAGGGGCTC 576
OY 60 ProAspArgPheSerGlySerIlySerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
   |||
Db 577 CTGACCGATTTCTTGCTCCAAAGTGGACCTCAGCTTCCCTGCGCATCAGTGGGCTC 636
OY 80 ArgSerGluAspGluAlaAspTyRyCySaIaAlaIleTrpAspAspSerLeuSerGlyTrp 99
   |||
Db 637 CGGTCGAGAGATGAGGCTGATTATTACTGTGCGGCTTCGTGATGACACTCTCGGTATG 696
OY 100 ValPheGlyGlyGlyThrIlySerLeuThrValLeuGly 111
   |||
Db 697 GTGTTGCGGAGAGAACCAAGCTGAGCGGTCTAGGT 732
```

RESULT 8

US-10-503-433B-20

```
; Sequence 20, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 20
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-12
US-10-503-433B-20
```

Pred. No.:	3,35e-43	Length:	803
Score:	466.50 <td>Matches:</td> <td>94</td>	Matches:	94
Percent Similarity:	88.5% <td>Conservative:</td> <td>6</td>	Conservative:	6
Best Local Similarity:	83.2% <td>Mismatches:</td> <td>11</td>	Mismatches:	11
Query Match:	79.3% <td>Indels:</td> <td>2</td>	Indels:	2
DB:	6 <td>Gaps:</td> <td>1</td>	Gaps:	1

US-10-092-640-36 (1-111) x US-10-503-433B-20 (1-803)

```
OY 1 GlnSerValIleuThrGlnProSerValSerAlaAlaProGlyGlnIlyValThrIle 20
   |||
Db 397 CAGTCTGTGCTACTCAGCCACCTCAGGCTCTGGAGACCCCGGAGAGGGTCAACATC 456
OY 21 SerCySerGlySerSerSerSerAniIleGlyAsnAsnTyR---ValSerTrpYrGlnGln 39
   |||
Db 457 TCTTGCACTGGAGAGAGCTCCCAACATCGGGGAGGTTTGTGATGATTAAGTATCAGCAG 516
OY 40 LeuProGlyThrAlaProIlySerLeuLeuIleTyRgIlyHisThrAsnArgProAlaGlyVal 59
   |||
Db 517 CTCCGAGGAAACGGCCCAACTCCTCATCTATGTGTACAAACATCGGCCCTCAGGGGCTC 576
OY 60 ProAspArgPheSerGlySerIlySerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
   |||
Db 577 CTGACCGATTTCTTGCTCCAAAGTGGACCTCAGCTTCCCTGCGCATCAGTGGGCTC 636
OY 80 ArgSerGluAspGluAlaAspTyRyCySaIaAlaIleTrpAspAspSerLeuSerGlyTrp 99
   |||
Db 637 CGGTCGAGAGATGAGGCTGATTATTACTGTGCGGCTCATGATGACATCATTAAGGGTGC 696
OY 99 PValPheGlyGlyGlyThrIlySerLeuThrValLeuGly 111
   |||
Db 697 GGTGTTGCGGAGAGCAACCAAGCTGAGCGGTCTAGGT 733
```

```
RESULT 9
US-10-503-433B-21
; Sequence 21, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWinn9
; SEQ ID NO 21
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-15
US-10-503-433B-21

Alignment Scores:
Pred. No.: 4,2e-42 Length: 792
Score: 456.50 Matches: 93
Percent Similarity: 90.2% Conservative: 8
Best Local Similarity: 83.0% Mismatches: 10
Query Match: 77.6% Indels: 2
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-21 (1-792)
QY 1 GlnSerValleuthrGlnProPserValSerAlaAlaProGlyGlnLysValThrIle 20
Db 396 CAGTCTGTGCTGACTGACCACTCAGCCTCTGGGACCCCGGCGAGAGGTCACCATC 455
QY 21 SerCySerGlySerSerSerAenIleGlyAsnAsnTyr--ValSerTPYrGlnGln 39
Db 456 TCTTGACACTGGGAGAGCTCCACATCGGGGAGAGTATGATGATACCTGATCAGCAG 515
QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
Db 516 CTCGCCAGAACGGCCCCCAAACTCTCATCTATGTAACAACAATCGGCCCTCAGGGGTC 575
QY 60 ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
Db 576 CCGACCGCATTCCTCTGCTCCAGCTCGGACCTCGACCTCCCTGGCCATCAGTGGGCTC 635
QY 80 ArgSerGluAspGluAlaAspTyrTyrCyAsnAlaAlaTrpAspAspSerLeuSerGlyTyr 99
Db 636 CGGTCCGAGAGATGAGGCTGATTATTACTGTGGCGGCTTTGATGACACCATTAATGTGCC 695
QY 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 696 GTGTTCGGCGAGAGAAC-AAAGCTGACGAGCTCTAAGT 730

RESULT 10
US-10-503-433B-18
; Sequence 18, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
```

```
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWinn9
; SEQ ID NO 18
; LENGTH: 779
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-1
US-10-503-433B-18

Alignment Scores:
Pred. No.: 6,84e-42 Length: 779
Score: 454.50 Matches: 94
Percent Similarity: 88.4% Conservative: 5
Best Local Similarity: 83.9% Mismatches: 12
Query Match: 77.3% Indels: 2
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-18 (1-779)
QY 1 GlnSerValleuthrGlnProPserValSerAlaAlaProGlyGlnLysValThrIle 20
Db 397 CAGTCTGTGCTGACTGACCACTCAGCCTCTGGGACCCCGGCGAGAGGTCACCATC 456
QY 21 SerCySerGlySerSerSerAenIleGlyAsnAsnTyr--ValSerTPYrGlnGln 39
Db 457 TCTTGACACTGGGAGAGCTCCACATCGGGGAGAGTATGATGATACCTGATCAGCAG 516
QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
Db 517 CTCGCCAGAACGGCCCCCAAACTCTCATCTATGTAACAACAATCGGCCCTCAGGGGTC 576
QY 60 ProAspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
Db 577 CCGACCGCATTCCTCTGCTCCAGCTCGGACCTCGACCTCCCTGGCCATCAGTGGGCTC 636
QY 80 ArgSerGluAspGluAlaAspTyrTyrCyAsnAlaAlaTrpAspAspSerLeuSerGlyTyr 99
Db 637 CGGTCCGAGAGATGAGGCTGATTATTAAGT-GCGGCTCAGCATGAGCGCCCTAAGCCGATCC 695
QY 100 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 111
Db 696 GTGTTCGGCGAGAGAACCAAGCTGACGAGCTCTAAGT 731

RESULT 11
US-11-254-679-31
; Sequence 31, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Kienner, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyne, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMGBl and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 31
```

```
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-254-679-31

Alignment Scores:
Pred. No.: 4.28e-42 Length: 333
Score: 452.00 Matches: 88
Percent Similarity: 87.3% Conservative: 8
Best Local Similarity: 80.0% Mismatches: 14
Query Match: 76.9% Indels: 0
DB: 7 Gaps: 0

US-10-092-640-36 (1-111) x US-11-254-679-31 (1-333)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
Db 4 CAGAGCGAATTGACTCAGCCACCTCGGTGTGAAGCCCGGGCGAGGGGTCAACATC 63

QY 21 SerCySerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTriPyrGlnGln 40
   |||||
Db 64 TCTGTGTTCTGGAAGACCTCCAAACATCGAATAATATGCTGTATCTGTAACAGACGCTC 123

QY 41 ProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyValPro 60
   |||||
Db 124 CCAGAGAAAGCTCCCAAACCTCCATCTATATGATGATCTGCTGCCCTCAGGGGTCTCT 183

QY 61 AspaArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPheArg 80
   |||||
Db 184 GACCAATTTCTGGCTCCAAAGTCTGGCACTCAGGCTCCCTGGCCATCAGTGGGCTCCAG 243

QY 81 SerGluAspGluAlaAspTyrTyrCysAlaAlaATPAspAspSerLeuSerGlyTyrVal 100
   |||||
Db 244 TCTGAGGATGAGAGCTGACTATTAATCTGATCATGGATGACAGCACTGAATGTCGCTG 303

QY 101 PheGlyGlyGlyThrLysLeuThrValLeu 110
   |||||
Db 304 TTCGGCGAGGAGGACCAAGTTGACCGCTCTA 333

RESULT 12
US-10-503-433B-22
; Sequence 22, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 22
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-20
US-10-503-433B-22

Alignment Scores:
Pred. No.: 1.33e-41 Length: 722
Score: 451.50 Matches: 91
Percent Similarity: 89.9% Conservative: 7
Best Local Similarity: 83.5% Mismatches: 10
Query Match: 76.8% Indels: 2
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-22 (1-722)
```

```
QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
Db 396 CAGTCTGCTGCTACTCAGCCACCTCAGCGTTGGAGACCCCGGGCGAGGGGTCAACATC 455

QY 21 SerCySerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTriPyrGlnGln 39
   |||||
Db 456 TCTTCCACTGGGAGAGAGCTCCAAACATCGGGGCGAGGTACGAGTACACTGATACAGCAG 515

QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
   |||||
Db 516 CTCGAGAGAACGGCCCCCAAACCTCCTCATATGATGTAACAAATCGGCGCTCAGGGGCTC 575

QY 60 ProAspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
   |||||
Db 576 CCTGACCAATTTCTGGCTCCAAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGGCTC 635

QY 80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaATPAspAspSerLeuSerGlyTyr 99
   |||||
Db 636 CGGTCCGAGATGAGAGCTGATTAATTAATGTCGGCTTATGATGACAGATATGATGTCAG 695

QY 100 ValPheGlyGlyGlyThrLysLeuThr 108
   |||||
Db 696 GTTTCGGCGGAGA-ACCAAGCTGACG 721

RESULT 13
US-10-503-433B-17
; Sequence 17, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 17
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-20
US-10-503-433B-17

Alignment Scores:
Pred. No.: 7.67e-41 Length: 706
Score: 444.50 Matches: 86
Percent Similarity: 89.3% Conservative: 6
Best Local Similarity: 83.5% Mismatches: 10
Query Match: 75.6% Indels: 1
DB: 6 Gaps: 1

US-10-092-640-36 (1-111) x US-10-503-433B-17 (1-706)

QY 1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20
   |||||
Db 397 CAGTCTGCTGCTACTCAGCCACCTCAGCGTTGGAGACCCCGGGCGAGGGGTCAACATC 456

QY 21 SerCySerGlySerSerSerAsnIleGlyAsnAsnTyrValSerTriPyrGlnGln 39
   |||||
Db 457 TCTTCCACTGGGAGAGAGCTCCAAACATCGGGGCGAGGTATGATGTAACACTGATACAGCAG 516

QY 40 LeuProGlyThrAlaProLysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
   |||||
Db 517 CTCGAGAGAACGGCCCCCAAACCTCCTCATATGATGTAACAAATCGGCGCTCAGGGGCTC 576

QY 60 ProAspArgPheSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
   |||||
Db 577 CTTGACCAATTTCTGGCTCCAAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGGCTC 636
```

```
QY      80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTrp 99
      |||
Db      637 CGGTCCGAGATAGAGCTGATTATTACTGTGGCTTACGATGACGGCCCTAAGCTGAGT 696
QY      100 ValPheGly 102
      |||
Db      697 GTCTTCGGC 705

RESULT 14
US-10-503-433B-15
; Sequence 15, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 15
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 1-10
US-10-503-433B-15

Alignment Scores:
Pred. No.:      5,86e-40      Length:      704
Score:          436.50      Matches:      84
Percent Similarity: 90.2%      Conservative: 8
Best Local Similarity: 82.4%      Mismatches: 9
Query Match:    74.2%      Indels:      1
DB:             Gaps:      1

US-10-092-640-36 (1-111) x US-10-503-433B-15 (1-704)
QY      1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20
      |||
Db      397 CAGTCTGTGTGCTGCTAGCCACCTCAGCGCTGGGACCCCGGCGAGAGGTCACCATC 456
QY      21 SerCySerGlySerSerSerSerAlaIleGlyAsnAsnTyr---ValSerTpyTyrGlnGln 39
      |||
Db      457 TCTTGACACTGGAGGACGCTCCAAACATCGGGGCAAGTTATGATGATATGCTGGTATCAGCAG 516
QY      40 LeuProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
      |||
Db      517 CTCCCGAGAACGGCCCCCAACTCCTCATCTATGTAACAACAATCGGCCCTCAGGGGCTC 576
QY      60 ProAspArgPheSerSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
      |||
Db      577 CCGACCGAATTCCTGTGGCTCCCAAGTCTGGACCTCGACCTCCCTGGCCATCAGTGGGCTC 636
QY      80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTrp 99
      |||
Db      637 CGGTCCGAGATAGAGCTGATTATTACTGTGGCTTACGATGACGGCCCTAAGCTGAGT 696
QY      100 ValPhe 101
      |||
Db      697 GTCTTC 702

RESULT 15
US-11-154-103-29
; Sequence 29, Application US/11154103
; Publication No. US20060099205A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
```

```
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-0004200S
; CURRENT APPLICATION NUMBER: US/11/154,103
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US10/406,830
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-11-154-103-29

Alignment Scores:
Pred. No.:      1,45e-39      Length:      864
Score:          434.00      Matches:      84
Percent Similarity: 86.6%      Conservative: 13
Best Local Similarity: 75.0%      Mismatches: 13
Query Match:    73.8%      Indels:      2
DB:             Gaps:      2

US-10-092-640-36 (1-111) x US-11-154-103-29 (1-864)
QY      1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnIysValThrIle 20
      |||
Db      463 CAGTCTGTGTGAGCCAGCGCCCTCGTATCTGGGGCCCCCAGGCGAGAGGTCACCATC 522
QY      21 SerCySerGlySerSerSerSerAlaIleGlyAsnAsnTyr---ValSerTpyTyrGlnGln 39
      |||
Db      523 TCCTGCACTGGGAGGACGCTCCAAACATCGGGGCAAGTTTGTATGATGATACGTGTACAGCA 582
QY      40 LeuProGlyThrAlaProIysLeuLeuIleTyrGlyHisThrAsnArgProAlaGlyVal 59
      |||
Db      583 CTTCAGGAACAGCCCCCAACTCCTCATCTATGTAACAACAATCGGCCCTCAGGGGCTC 642
QY      60 ProAspArgPheSerSerGlySerIysSerGlyThrSerAlaSerLeuAlaIleSerGlyPhe 79
      |||
Db      643 CCGACCGAATTCCTGCTCCCTCCAAAGTCTGGACCTCAGCCTCCCTGGGCATCACCGACTC 702
QY      80 ArgSerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTrp 99
      |||
Db      703 CAGATCGGGGACCAAGCCGATTATTACTGGGCTCATATACAGCACCTACTCT---TGG 759
QY      100 ValPheGlyGlyIleThrIysLeuThrValIleGly 111
      |||
Db      760 GTCTTCGGGAGGAGCAAGGTCACCGTCTTAGT 795

Search completed: May 25, 2006, 21:28:33
Job time : 20.575 secs
```

This Page Blank (uspro)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 25, 2006, 16:11:24 ; Search time 4911.14 Seconds
(without alignments)
2519.344 Million cell updates/sec

Title: US-10-092-640-32

Perfect score: 700

Sequence: 1 GVQLQSGALKKPGESLKI.....AKMPEYFGMGQTLVTYSS 129

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 segs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=xlh
-Q=/abs/ABSSWEB.spool/US10092640/runat.25052006.155713.5836/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEA SIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=LOCAL
-USER=US10092640@CCN1_1.5767@runat.25052006.155713.5836 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:.*
1: gb_env:.*
2: gb_pat:.*
3: gb_ph:.*
4: gb_pl:.*
5: gb_pr:.*
6: gb_ro:.*
7: gb_sts:.*
8: gb_sy:.*
9: gb_un:.*
10: gb_vi:.*
11: gb_ov:.*
12: gb_ncg:.*
13: gb_in:.*
14: gb_cm:.*
15: gb_ba:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	700	100.0	387	5 HSNJ6542	U36542 Human anti-
2	700	100.0	387	5 HSNJ8338	U38338 Human anti-
3	700	100.0	387	5 HSNJ8331	U38331 Human anti-

Result No.	Score	Query Match	Length	DB ID	Description
4	700	100.0	387	5 HSNJ8332	U38332 Human anti-
5	700	100.0	774	2 AR083879	AR083879 Sequence
6	700	100.0	774	2 AR278815	AR278815 Sequence
7	697	99.6	1509	8 AF516873	AF516873 Synthetic
8	694	99.1	387	5 HSNJ8333	U38333 Human anti-
9	692	98.9	387	5 HSNJ8330	U38330 Human anti-
10	689	98.4	387	5 HSNJ8224	U38224 Human anti-
11	688	98.3	387	5 HSNJ8223	U38223 Human anti-
12	684	97.7	387	5 HSNJ8329	U38329 Human anti-
13	683	97.6	387	5 HSNJ8327	U38327 Human anti-
14	683	97.6	387	5 HSNJ8334	U38334 Human anti-
15	682	97.4	387	5 HSNJ6543	U36543 Human anti-
16	680	97.1	387	5 HSNJ8336	U38336 Human anti-
17	669	95.6	387	5 HSNJ6552	U36552 Human anti-
18	669	95.6	387	5 HSNJ6557	U36557 Human anti-
19	669	95.6	387	5 HSNJ8334	U38334 Human anti-
20	666	95.1	387	5 HSNJ6544	U36544 Human anti-
21	666	95.1	387	5 HSNJ6547	U36547 Human anti-
22	663	94.7	387	5 HSNJ6550	U36550 Human anti-
23	663	94.7	387	5 HSNJ6551	U36551 Human anti-
24	663	94.7	387	5 HSNJ6554	U36554 Human anti-
25	661	94.4	387	5 HSNJ6559	U36559 Human anti-
26	659	94.1	387	5 HSNJ6559	U36559 Human anti-
27	658	94.0	387	5 HSNJ6556	U36556 Human anti-
28	657	93.9	387	5 HSNJ6546	U36546 Human anti-
29	656	93.7	387	5 HSNJ6535	U36535 Human anti-
30	655	93.6	387	5 HSNJ6548	U36548 Human anti-
31	648	92.6	387	5 HSNJ8325	U38325 Human anti-
32	646	92.3	387	5 HSNJ6545	U36545 Human anti-
33	645	92.1	387	5 HSNJ6553	U36553 Human anti-
34	639	91.3	387	5 HSNJ6555	U36555 Human anti-
35	629	89.9	387	2 AX112648	AX112648 Sequence
36	629	89.9	387	2 HSNJ6558	U36558 Human anti-
37	545.5	77.9	372	2 AB063897	AB063897 Homo sapi
38	540	77.1	364	2 DD186925	DD186925 Method fo
39	539	77.0	906	2 AX111698	AX111698 Sequence
40	539	77.0	498	5 AY393196	AY393196 Homo sapi
41	537	76.7	375	5 AB067159	AB067159 Homo sapi
42	534	76.3	381	5 AF110484	AF110484 Homo sapi
43	531.5	75.9	381	5 AF174110	AF174110 Homo sapi
44	530.5	75.8	367	5 AF174110	AF174110 Homo sapi
45	530.5	75.8	378	5 HSNJ7538	U77538 Human clone

ALIGNMENTS

RESULT 1
HSNJ6542
LOCUS Human anti-c-erbB-2 immunoglobulin heavy chain V region mRNA,
DEFINITION partial cds.
ACCESSION U36542
VERSION U36542.1 GI:1145223
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE Schier,R., Bye,J., Apell,G., McCall,A., Adams,G.P., Weiner,L.M. and
Marks,U.D.
TITLE Isolation of high affinity monomeric Human anti-c-erbB-2 single
chain Fv using affinity driven selection
J. Mol. Biol. (1995) In press
REFERENCE J. Mol. Biol. (1995) In press
AUTHORS Schier,R.
TITLES Direct Submission
JOURNAL Submitted (18-SEP-1995) Robert Schier, Anesthesia, University of
California at San Francisco, 1001 Potrero Avenue, San Francisco, CA
94110, USA
FEATURES
source Location/Qualifiers
1..387

CDS

```
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C6.5"
<1..>387
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin heavy chain V
region"
/protein_id="AA085074.1"
/db_xref="GI:1145224"
/translation="OVQLQSGAEILKKGESLKISCKSGSYFTSYWIAMWRMPGKG
LEYMGLIYPGSDPTKYSRPSFOGOVTISVDKSVSTAYVLQWSSLKPSDSAVYFCARHDVG
YCSSSNCAKMPBYFQHWGQGLVTYSS"
```

ORIGIN

Alignment Scores:

```
Pred. No.: 4.77e-76 Length: 387
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0
```

US-10-092-640-32 (1-129) x HSU36542 (1-387)

```
QY 1 GlnValGlnLeuLeuGlnSerGlyValAGluLeuLysLysProGlyGlnSerLeuLysIle 20
    |||
DB 1 CAGGTGCACACTGTGTGACGTCTGGGGCAGAGTTGAAAAACCCGGGAGACTCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTrpValArgIleMet 40
    |||
DB 61 TCTCTGAAGGGTTCTGGATACAGCTTACCAAGTACTGATCGCTGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
    |||
DB 121 CCCGGGAAAGCCTGGAGTACATGGGGCTCATCTATCTGAGTACTGACACCAATATC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
    |||
DB 181 AGCCCGTCTCTCCAAAGCCAGGTCACCACTCAGTGCAGCAAGTCCGTCAAGCACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
    |||
DB 241 TTGCATATGAGCAGATGTGAAGCCTTCGACAGGCCCGGTATTTTGTGCGACACTGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
    |||
DB 301 GTGGGATATTGCAAGTATTCCAACTGCGCAAGTGGCTGGAATACTTCCAGCATTTGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
    |||
DB 361 CAGGGCACCCCTGTGTCACGCTCTCTCA 387
```

RESULT 2

HSU38328

LOCUS HSU38328 387 bp mRNA linear PRI 02-OCT-1996

DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,

clone C6PM7.

ACCESSION U38328

VERSION U38328.1 GI:1145317

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE

1 (bases 1 to 387)

Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and

AUTHORS

TITLE

Identification of functional and structural amino-acid residues by

JOURNAL

PUBMED

REFERENCE 2 (bases 1 to 387)

AUTHORS

Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and

Marks,J.D.

TITLE

Direct Submission

JOURNAL

Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San

Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA

FEATURES

source

1..387

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="C6PM7"

/clone_lib="semisynthetic scFv phage display library"

<1..>387

/codon_start=1

/product="anti-c-erbB-2 immunoglobulin heavy chain V"

/protein_id="AA085074.1"

/db_xref="GI:1145318"

/translation="OVQLQSGAEILKKGESLKISCKSGSYFTSYWIAMWRMPGKG

LEYMGLIYPGSDPTKYSRPSFOGOVTISVDKSVSTAYVLQWSSLKPSDSAVYFCARHDVG

YCSSSNCAKMPBYFQHWGQGLVTYSS"

ORIGIN

Alignment Scores:

```
Pred. No.: 4.77e-76 Length: 387
Score: 700.00 Matches: 129
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0
```

US-10-092-640-32 (1-129) x HSU38328 (1-387)

```
QY 1 GlnValGlnLeuLeuGlnSerGlyValAGluLeuLysLysProGlyGlnSerLeuLysIle 20
    |||
DB 1 CAGGTGCACACTGTGTGACGTCTGGGGCAGAGTTGAAAAACCCGGGAGACTCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTyrIleAlaTrpValArgIleMet 40
    |||
DB 61 TCTCTGAAGGGTTCTGGATACAGCTTACCAAGTACTGATCGCTGGGTGGCCAGATG 120
QY 41 ProGlyLysGlyLeuGlnLysMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
    |||
DB 121 CCCGGGAAAGCCTGGAGTACATGGGGCTCATCTATCTGAGTACTGACACCAATAT 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
    |||
DB 181 AGCCCGTCTCTCCAAAGCCAGGTCACCACTCAGTGCAGCAAGTCCGTCAAGCACTGCTTAC 240
QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
    |||
DB 241 TTGCATATGAGCAGATGTGAAGCCTTCGACAGGCCCGGTATTTTGTGCGACACTGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
    |||
DB 301 GTGGGATATTGCAAGTATTCCAACTGCGCAAGTGGCTGGAATACTTCCAGCATTTGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
    |||
DB 361 CAGGGTACCCCTGTGTCACGCTCTCTCA 387
```

RESULT 3

HSU38331

LOCUS HSU38331 387 bp mRNA linear PRI 02-OCT-1996

DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V-gene, clone

C6PM10.

ACCESSION U38331

VERSION U38331.1 GI:1145323

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis
 JOURNAL Gene 169 (2), 147-155 (1996)
 PUBMED 8647439
 REFERENCE 2 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Direct Submision
 JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 FEATURES
 source
 1..387
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="C6PM10"
 /clone_lib="semisynthetic scFv phage display library"
 <1..>387
 /codon_start=1
 /product="anti-c-erbB-2 immunoglobulin heavy chain V"
 /protein_id="AAB09641.1"
 /db_xref="GI:1145324"
 /translation="QVQLQSGAELEKPKESLKISCKSGSYFTSYWIMVRQMPKG LEYMGILYPGSDTKYSPFQGVITISVSKSVSTAYLQWSLSKPSDAVYFCARHDVG YCSSNCAKMPYFQHWGGLTVTVSS"
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,77e-76 Length: 387
 Score: 700.00 Matches: 129
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0
 US-10-092-640-32 (1-129) x HSU38331 (1-387)
 QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
 Db 1 CAGGTCACACTGTTGCAAGTCTGGGGCAGAGTTGAAGAGCCGGGAGTCTCTGAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
 Db 61 TCTGTGAAGGTTCTGATACAGCTTTACAGCTACTGATGCTGGGTGGGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
 Db 121 CCCGGGAAAGGCTGGAAGTACATGGGGCTCATCTATCCGTGACCTCTACACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 AGCCGCTCTTCCAGAGCCAGGTACCACTCTCATGACAAAGTCCCTCCAGCACTGCTTAC 240
 QY 81 LeuGlnTyrSerSerLeuLysPheSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 TTGCATATGAGCAGTCTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
 Db 301 GTGGGATATTCAGATGATTCCTCAAGTGGCGAAAGTGGCTGAATATCTTCAGCATTTGGGGC 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 361 CAGGATACCTGTCTCCTCTCTCA 387
 RESULT 4
 HSU38332 387 bp mRNA linear PRI 02-OCT-1996
 LOCUS
 DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V-gene; clone

CGPM11.
 ACCESSION U38332
 VERSION U38332.1 GI:1145325
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis
 JOURNAL Gene 169 (2), 147-155 (1996)
 PUBMED 8647439
 REFERENCE 2 (bases 1 to 387)
 AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
 TITLE Direct Submision
 JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
 FEATURES
 source
 1..387
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="C6PM11"
 /clone_lib="semisynthetic scFv phage display library"
 <1..>387
 /codon_start=1
 /product="anti-c-erbB-2 immunoglobulin heavy chain V"
 /protein_id="AAB09642.1"
 /db_xref="GI:1145326"
 /translation="QVQLQSGAELEKPKESLKISCKSGSYFTSYWIMVRQMPKG LEYMGILYPGSDTKYSPFQGVITISVSKSVSTAYLQWSLSKPSDAVYFCARHDVG YCSSNCAKMPYFQHWGGLTVTVSS"
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,77e-76 Length: 387
 Score: 700.00 Matches: 129
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0
 US-10-092-640-32 (1-129) x HSU38332 (1-387)
 QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGlnSerLeuLysIle 20
 Db 1 CAGGTCACACTGTTGCAAGTCTGGGGCAGAGTTGAAGAGCCGGGAGTCTCTGAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
 Db 61 TCTGTGAAGGTTCTGATACAGCTTTACAGCTACTGATGCTGGGTGGGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
 Db 121 CCCGGGAAAGGCTGGAAGTACATGGGGCTCATCTATCCGTGACCTCTACACCAATAC 180
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 181 AGCCGCTCTTCCAGAGCCAGGTACCACTCTCATGACAAAGTCCCTCCAGCACTGCTTAC 240
 QY 81 LeuGlnTyrSerSerLeuLysPheSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
 Db 241 TTGCATATGAGCAGTCTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
 Db 301 GTGGGATATTCAGATGATTCCTCAAGTGGCGAAAGTGGCTGAATATCTTCAGCATTTGGGGC 360

[illegible]

AUTHORS	Marks, J.D. and Schier, R.		
TITLE	High affinity human antibodies to tumor antigens		
JOURNAL	Patent: US 6512097-A 4 28-JAN-2003; The Regents of the University of California; Oakland, CA		
FEATURES	location/Qualifiers		
source	1..774 /organism="unknown" /mol_type="genomic DNA"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1,15e-75	length:	774
Score:	700.00	Matches:	129
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0
US-10-092-640-32 (1-129) x AR278815 (1-774)			
QY	1	GlnValGlnIleuLeuGlnSerGlyAlaGlnIleuLysPheGlyIuSerIleuLysIle	20
Db	1	CAGGTGCAGCGCTTGTCAGCTCTGGGGGCAGAGTTGAAAAACCCGGGAGCTCTGGAAGATC	60
QY	21	SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValaGlnMet	40
Db	61	TCCGTGAAGGGTTCTCGATACAGCTTTACACGATACGATCGCTGGGGCCGAGATG	120
QY	41	ProGlyIysGlyLeuGlnIuTyrMetGlyLeuIleTyrProGlyIysPheSerPThrLysTyr	60
Db	121	CCCCGAAAGGCTTGGAGTACATGGGGCTCATCTTCTGTGACTTGACACCAATAC	180
QY	61	SerProSerPheGlnGlyGlnValThrIleSerValaLysSerValaSerThrAlaTyr	80
Db	181	AGCCCGCTCTTCCAGGCGCAGGTACCATCTCAGTGCACAAAGTCCGTCAGCATCGCTAC	240
QY	81	LeuGlnTrpSerSerIleuLysPheSerAspSerAlaValTyrPheCysAlaIghIAsp	100
Db	241	TTGCAGATGGAGCAGACTCTGAAGCCCTCGGACAGCGCCCTGTATTGTTGTGGAGACATGAC	300
QY	101	ValGlyTyrCysSerSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly	120
Db	301	GTGGGAATTTGCAATGATCTCCAACTGGGCAGAAAGTGGCTTAATCTTCCAGCATTTGGGCG	360
QY	121	GlnGlyThrIleuValThrValSerSer	129
Db	361	CAGGCGACCTCGTCAACGCTCTCCTCA	387
RESULT 7			
AF516873	1509 bp	mRNA	linear
LOCUS	AF516873		SYN 01-MAR-2004
DEFINITION	Synthetic construct membrane-acting immunotoxin fusion protein		
VERSION	mRNA, complete cds.		
ACCESSION	AF516873		
KEYWORDS	AF516873.1 GI:31324248		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	1 (bases 1 to 1509)		
TITLE	Gurkan,C. and Ellar,D.J.		
JOURNAL	Design and construction of membrane-acting immunotoxins based on		
REFERENCE	the Bacillus thuringiensis delta-endotoxin Cyt2Aa1 for expression		
AUTHORS	in Pichia pastoris		
TITLE	Med. Microbiol. Immunol. (Berl.) 189, 37-37 (2000)		
JOURNAL	2 (bases 1 to 1509)		
REFERENCE	Gurkan,C. and Ellar,D.J.		
AUTHORS	Expression in Pichia pastoris and purification of a membrane-acting		
TITLE	immunotoxin based on a synthetic gene coding for the Bacillus		
JOURNAL	thuringiensis Cyt2Aa1 toxin		
REFERENCE	Protein Expr. Purif. 29 (1), 103-116 (2003)		
PUBMED	12729731		
REFERENCE	3 (bases 1 to 1509)		

AUTHORS Gurkan, C. and Ellar, D.J.
TITLE Expression of the Bacillus thuringiensis Cyt2Aa1 toxin in Pichia pastoris using a synthetic gene construct
JOURNAL Biotechnol. Appl. Biochem. 38 (Pt 1), 25-33 (2003)
PUBMED 12628007
REFERENCE 4 (bases 1 to 1509)
AUTHORS Gurkan, C., Ellar, D.J. and Marks, J.
TITLE Direct Submision
JOURNAL Submitted (30-MAY-2002) Department of Biochemistry, University of Cambridge, 80 Tennis Court Road, Old Addenbrooke's Site, Cambridge CB2 1QA, England

FEATURES
source
 1..1509
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
source
 13..780
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 841..1440
 /organism="Bacillus thuringiensis serovar kyushuensis"
 /mol_type="mRNA"
 /serovar="kyushuensis"
 /db_xref="taxon:44161"
 10..1509
 /note="IT-A; human scFv fragment C6.5 fused to activated form of the Bacillus thuringiensis serovar kyushuensis Cyt2Aa1 toxin, joined together by a serine/glycine linker"
 /codon_start=1
 /transl_table=11
 /product="membrane-acting immunotoxin fusion protein"
 /protein_id="AAP47198.1"
 /db_xref="GI:31324249"
 /translation="MSQVQLTQSGAEVKKRQDSGKLISQDGSYFTSYIAWVROMG KLEWGLIYPGDSITKYSFSGQVITISDVSTAYLQMSIKRSDSAVYFCARHD VQYSSSNCAKMPYEQHWGCTLVTVSSGGSGSGSGSGSGSVLTQPSVSAAP GOKVTISCGSSSNIGNNIVSMYQQLPGTAPKLLYGHNNRPGVDRSGSKGTSIA SAISGFRSEDEADYICAMWDSLGSWVGSGGKTLVGLIESGGSGSGSGSGSGSP RSDLNFTNFTVYVQPOYINQALFLANAFQGAIDPLNFTNFEKALQIANGIPNSAIVK TLNQSIVTQVTEISVMFQELKKIIOELVGLINSTFNNSEATIKGTFTNIDTOIDE AWIPWMSLSNHTSYVYNIPLFSLINEDTGAVAVLPLAEVSVDEVKQVLFPTIKDS ARVEYKAKLTVLQALHSSNAIYVDIFLEOKLISEEDLNSAVDHHHHHH"
 787..834
 /note="serine/glycine linker"

ORIGIN
 misc_feature
 Alignment Scores:
 Pred. No.: 6,25e-75 Length: 1509
 Score: 697.00 Matches: 128
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 99.2% Mismatches: 0
 Query Match: 99.6% Indels: 0
 DB: 8 Gaps: 0

US-10-092-640-32 (1-129) x AF516873 (1-1509)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysPProGlyGluSerLeuLysIle 20
 Db 16 CAGGTGCACGCTGTTCAGCTGGGGCAGAGGTGAAGAAACCCGGGAGCTCTGAAGATC 75
 QY 21 SerCySLySGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 Db 76 TCCTGTAAAGGTTCTCGATACAGCTTACCACTACGTGATCGCTGGCGCCAGATG 135
 QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuLysIleTyrProGlyLysAspSerPheThrLysTyr 60
 Db 136 CCCGGGAAAGCCCTGGAGTACATGGGGCTCATCTATCTCGGTGACTCTACACCAATATC 195
 QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 Db 196 ACCCGCTCTTCCAAAGGCCAGGTCAACCATCTCAGTGCACAGTCCCTCAGCACTGCTAC 255

QY 81 LeuGlnTyrSerSerLeuLysPProSerAlaValTyrPheCysAlaAaGHisAsp 100
 Db 256 TTGCATATGAGCAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGGAACATGAC 315
 QY 101 ValGlyTyrCySerSerSerSerAaenCysAlaValTyrProGluTyrPheGlnHsIleTPGly 120
 Db 316 GTGGGATATTCGATGTTGTTCCACTGCGCAAGTGGCTGTAATATTCACGATTGGGGC 375
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 Db 376 CAGGCACCCCTGCTGACCGCTCCTCA 402

RESULT 8
HSU38333
LOCUS
DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V-gene; clone
ACCESSION U38333
VERSION U38333.1 GI:1145327
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Schier, R., Ballint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis
JOURNAL Gene 169 (2), 147-155 (1996)
PUBMED 8647439
REFERENCE 2 (bases 1 to 387)
AUTHORS Schier, R., Ballint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
TITLE Direct Submision
JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
source
 1..387
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C6PM12"
 /clone_1ib="semisynthetic scFv phage display library"
 <1..>387
 /codon_start=1
 /product="anti-c-erbB-2 immunoglobulin heavy chain V"
 /protein_id="AAB09643.1"
 /db_xref="GI:1145328"
 /translation="QVQLTQSGAEVKKRQDSGKLISQDGSYFTSYIAWVROMPGK LEWGLIYPGDSITKYSFSGQVITISDVSTAYLQMSIKRSDSAVYFCARHDV VQYSSSNCAKMPYEQHWGCTLVTVSS"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.59e-75 Length: 387
 Score: 694.00 Matches: 127
 Percent Similarity: 100.0% Conservative: 2
 Best Local Similarity: 98.4% Mismatches: 0
 Query Match: 99.1% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-32 (1-129) x HSU38333 (1-387)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysPProGlyGluSerLeuLysIle 20
 Db 1 CAGGTGCACGCTGTTCAGCTGGGGCAGAGGTGAAGAAACCCGGGAAATCTTGAAGATC 60
 QY 21 SerCySLySGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
 Db 61 TCCTGTAAAGGTTCTCGATACAGCTTACCACTACGTGATCGCTGGCGCCAGATG 120

```

QY      41  ProGlyLysGlyLeuGluuTyMetGlyLeuLeuTyProGlyAspSerAspThrLysTyR 60
Db      121  CCGGGGAAAGGCGCTGGAGTACATGGGGCTCATCTATCCGTGATTCCTATACCAATAC 180
QY      61  SerProSerPheGlnGlyGlnValThrLieserValAspLysSerValSerThrLysTyR 80
Db      181  ACCCGCTCTTCCAGAGCCAGGTGACCATCACAGTGAACAAGTCCCTCAGCACTGCTTAC 240
QY      81  LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
Db      241  TTGCATGAGAGCAGTCTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY      101  ValGlyTyrcysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db      301  GTGGGATATTTGACAGTATGTTCCAACTGCGCAAGTGCGCTGAATATCTTCAGCATTTGGGGC 360
QY      121  GlnGlyThrLeuValThrValSerSer 129
Db      361  CAGGGCACCCCTGGTCAACGCTCTCTCA 387

RESULT 9
HSU38330      387 bp  mRNA  linear  PRI 02-OCT-1996
LOCUS      Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,
DEFINITION  clone C6PM9.
ACCESSION  U38330
VERSION    U38330.1 GI:1145321
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 387)
REFERENCE  Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
            Identification of functional and structural amino-acid residues by
            parsimonious mutagenesis
            Gene 169 (2), 147-155 (1996)
            8647439
JOURNAL    PUBMED
PUBMED     2 (bases 1 to 387)
REFERENCE  Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
            Direct Submision
            Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
            Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
            source
            1..387
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="C6PM9"
            /clone_lib="semisynthetic scfv phage display library"
            <1..>387
            /codon_start=1
            /product="anti-c-erbB-2 immunoglobulin heavy chain V"
            /protein_id="AAB09640.1"
            /db_xref="GI:1145322"
            /translation="OVOLQSGAEVKKPGESLKISCKSGSGFTSYWIAWVROMPGKG
            LEYMLIYPGSDTKYSPSFOGVAITVYKSVSTAYLQWSLKPDSNAVYFCARHDVG
            YCSSNCAKMPYFQHWGQGLTVTVSS"

ORIGIN
Alignment Scores:
Pred. No.:      4,56e-75      Length:      387
Score:          692.00      Matches:      127
Percent Similarity: 99.2%      Conservative: 1
Best Local Similarity: 98.4%      Mismatches: 1
Query Match:    98.9%      Indels:      0
DB:             5      Gaps:      0
US-10-092-640-32 (1-129) x HSU38330 (1-387)

```

```

QY      1  GlnValGlnLeuLeuGlnSerGlyValGluLeuLysLysProGlyGluSerLeuLysIle 20
Db      1  CAGGTGACAGCTGTTTCAGTCTGGGGCAGAGTTGAAGAACCCGGGAGCTCTTGAAGATC 60
QY      21  SerCysLysGlySerGlyTyrcysSerPheThrSerSerTyrrPileAlaTriValArgGlnMet 40
Db      61  TCCTGTAAAGGTTCTCGATACAGCTTTTACAGACTTCTGATGCGCTGGGTGGCCAGATG 120
QY      41  ProGlyLysGlyLeuGluuTyMetGlyLeuLeuTyProGlyAspSerAspThrLysTyR 60
Db      121  CCGGGGAAAGGCGCTGGAGTACATGGGGCTCATCTATCCGTGATTCGATACCAATAC 180
QY      61  SerProSerPheGlnGlyGlnValThrLieserValAspLysSerValSerThrLysTyR 80
Db      181  ACCCGCTCTTCCAGAGCCAGGTGACCATCACAGTGAACAAGTCCCTCAGCACTGCTTAC 240
QY      81  LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyPheCysAlaArgHisAsp 100
Db      241  TTGCATGAGAGCAGTCTGAAGCCCTCGACAGCGCGGTGATTTTGTGCGAGACATGAC 300
QY      101  ValGlyTyrcysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db      301  GTGGGATATTTGACAGTATGTTCCAACTGCGCAAGTGCGCTGAATATCTTCAGCATTTGGGGC 360
QY      121  GlnGlyThrLeuValThrValSerSer 129
Db      361  CAGGGTACCCCTGGTCAACGCTCTCTCA 387

RESULT 10
HSU38224      387 bp  mRNA  linear  PRI 31-DEC-2001
LOCUS      Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds.
DEFINITION  U38224
ACCESSION  U38224
VERSION    U38224.1 GI:1145299
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 387)
REFERENCE  Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
            Identification of functional and structural amino-acid residues by
            parsimonious mutagenesis
            Gene 169 (2), 147-155 (1996)
            8647439
JOURNAL    PUBMED
PUBMED     2 (bases 1 to 387)
REFERENCE  Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and
AUTHORS    Marks, J.D.
            Direct Submision
            Submitted (07-OCT-1995) Ronert Schier, Anesthesia, UC San
            Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
            source
            1..387
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="C6PM1"
            /clone_lib="semisynthetic scfv phage display library"
            <1..>387
            /codon_start=1
            /product="anti-c-erbB-2 immunoglobulin heavy chain V"
            /protein_id="AAB84963.1"
            /db_xref="GI:1145300"
            /translation="OVOLQSGAEVKKPGESLKISCKSGSGFTSYWIAWVROMPGKG
            LEYMLIYPGSDTKYSPSOGVATISYDKSVSTAYLQWSLKPDSNAVYFCARHDVG
            YCSSNCAKMPYFQHWGQGLTVTVSS"

ORIGIN
Alignment Scores:
Pred. No.:      1,06e-74      Length:      387
Score:          689.00      Matches:      127

```

Percent Similarity: 99.2% Conservative: 1
 Best Local Similarity: 98.4% Mismatches: 1
 Query Match: 98.4% Indels: 0
 DB: 5 Gaps: 0

US-10-092-640-32 (1-129) x HSU38224 (1-387)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysProGlyGlnSerLeuLysIle 20
 DB 1 CAGGTGCAGCTGTTGACGCTGGGGCAGAGTAAAAAGCCGGGAGTCTCGAAGATC 60
 QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTripleAlaTrpValArgGlnMet 40
 DB 61 TCCTGTAAAGGTTCCGGATACAGCTTACAGCTACGATCCCTGGGTCGGCCAGATG 120
 QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
 DB 121 CCGGGAAAGGCTGGAGTACATGGGGCTCATCTATCTCTGATTCGTATACCAATAC 180
 QY 61 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
 DB 181 AGCCCTCTCTCCCAAGGCCAGGTCACATCTCAGTGCACAAGCCGTCAGCACTGCCTAC 240
 QY 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisasp 100
 DB 241 TTGCATGAGACGAGCTGTGAAGCCCTCGACAGCCCGCTGATTTTGTGGAGACATGAC 300
 QY 101 ValGlyTyrCysSerSerSerAsnGlyAlaLysTrpProGlyLysPheGlnHisTrpGly 120
 DB 301 GTGGGATATTGACAGTATTCACACTGCGCAAGTGGCTGAATATCTTCAGCATGGGGG 360
 QY 121 GlnGlyThrLeuValThrValSerSer 129
 DB 361 CAGGGCACCTGTGTCACCGTCTCTCA 387

RESULT 11

HSU38323

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

CDS

```

/db_xref="taxon:9606"
/clone_lib="C6PM8"
/clone_lib="semisynthetic scFv phage display library"
<1..>387
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin heavy chain V"
/protein_id="AAB09637.1"
/db_xref="GI:1145320"
/translation="QVQLQSGAELEKRRGSIKISKSGSYFTSYWIAWRQMPGK
LEWMLIYAGDSATKSPFQGVITISYDKSVIAYLQWSSLKPSDSAVYFCARDVG
YCSSNCAKMPYFQHWGQGLTVSS"

```

ORIGIN

Alignment Scores:

Pred. No.:	4,36e-74	Length:	387
Score:	684.00	Matches:	127
Percent Similarity:	98.4%	Conservative:	0
Best Local Similarity:	98.4%	Mismatches:	2
Query Match:	97.7%	Indels:	0
DB:	5	Gaps:	0

US-10-092-640-32 (1-129) x HSU38329 (1-387)

```

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
    |||||
DB 1 CAGGTGCACGCTTTGCAAGTCTGGGGCAGAGTTGAAGAAGCCGGGAGTCTTGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrrIleAlaTrpValArgGlnMet 40
    |||||
DB 61 TCCTGTAAAGGGTTCTGGATACAGCTTTACAGCTACTGGATCGCCGGGTGGCCGAGATG 120
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
    |||||
DB 121 CCCGGGAAAGGCTTGAGTACATGGGGCTCATCTATGCTGGCGATCTCTCCAAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
    |||||
DB 181 ACCCGGCTCTTCCAAAGGCCAGGTCACATCTCAGTCGACAGATCCGTCAGCACTGCTAC 240
QY 81 LeuGlnTrrPseSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
    |||||
DB 241 TTGCATATGAGAGAGTCTGAAGCCCTCGGACAGCGCGTGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrrProGlyTyrPheGlnHisTrrpGly 120
    |||||
DB 301 GTGGATATTTGCAAGTCTTCCAACTGCGAAAGTGGCTGAAATCTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
    |||||
DB 361 CAGGGTACCCCTGTGTACCGTCTCTCTCA 387

RESULT 13
HSU38327 387 bp mRNA linear PRI 02-OCT-1996
LOCUS Human anti-c-erbB-2 immunoglobulin heavy chain V mRNA, partial cds,
DEFINITION clone C6PM6.
ACCESSION U38327
VERSION U38327.1 GI:1145315
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 387)
Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and
Marks,J.D.
Identification of functional and structural amino-acid residues by
parthenonous mutagenesis
Gene 169 (2), 147-155 (1996)
JOURNAL PUBMED 8647439
REFERENCE 2 (bases 1 to 387)
AUTHORS Schier,R., Balint,R.F., McCall,A., Apell,G., Larrick,J.W. and

```

TITLE Marks J.D.
JOURNAL Direct Submission
 Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San
 Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
source location/Qualifiers
 1..387
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="C6PM6"
 /clone_lib="semisynthetic scFv phage display library"
 <1..>387
 /codon_start=1
 /product="anti-c-erbB-2 immunoglobulin heavy chain V"
 /protein_id="AAB09637.1"
 /db_xref="GI:1145316"
 /translation="QVQLQSGAELEKRRGSIKISKSGSYFTSYWIAWRQMPGK
 LEWMLIYAGDSATKSPFQGVITISYDKSVIAYLQWSSLKPSDSAVYFCARDVG
 YCSSNCAKMPYFQHWGQGLTVSS"

CDS

Alignment Scores:

Pred. No.:	5.77e-74	Length:	387
Score:	683.00	Matches:	126
Percent Similarity:	97.7%	Conservative:	0
Best Local Similarity:	97.7%	Mismatches:	3
Query Match:	97.6%	Indels:	0
DB:	5	Gaps:	0

ORIGIN

US-10-092-640-32 (1-129) x HSU38327 (1-387)

```

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysProGlyGluSerLeuLysIle 20
    |||||
DB 1 CAGGTGCACGCTTTGCAAGTCTGGGGCAGAGTTGAAGAAGCCGGGAGTCTTGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrrIleAlaTrpValArgGlnMet 40
    |||||
DB 61 TCCTGTAAAGGGTTCTGGATACAGCTTTACAGCTACTGGATCGCCGGGTGGCCGAGATG 120
QY 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyLysSerAspThrLysTyr 60
    |||||
DB 121 CCCGGGAAAGGCTTGAGTACATGGGGCTCATCTATGCTGGCGATTTATGTCGAGACATGAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
    |||||
DB 181 ACCCGGCTCTTCCAAAGGCCAGGTCACATCTCAGTCGACAGATCCGTCAGCACTGCTAC 240
QY 81 LeuGlnTrrPseSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
    |||||
DB 241 TTGCATATGAGAGAGTCTGAAGCCCTCGGACAGCGCGTGTATTTTGTGCGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrrProGlyTyrPheGlnHisTrrpGly 120
    |||||
DB 301 GTGGATATTTGCAAGTCTTCCAACTGCGAAAGTGGCTGAAATCTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
    |||||
DB 361 CAGGGTACCCCTGTGTACCGTCTCTCTCA 387

RESULT 14
HSU38334 387 bp mRNA linear PRI 02-OCT-1996
LOCUS Human anti-c-erbB-2 immunoglobulin heavy chain V-gene; clone
DEFINITION C6PM13.
ACCESSION U38334
VERSION U38334.1 GI:1145329
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 387)

```


AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
TITLE Identification of functional and structural amino-acid residues by parsimonious mutagenesis
JOURNAL Gene 169 (2), 147-155 (1996)
PUBMED 8647439
REFERENCE 2 (bases 1 to 387)
AUTHORS Schier, R., Balint, R.F., McCall, A., Apell, G., Larrick, J.W. and Marks, J.D.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1995) Robert Schier, Anesthesia, UC San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
source location/Qualifiers
1..387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CGPM13"
/clone_1lb="semisynthetic scFv phage display library"
CDS
<1..387
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin heavy chain v"
/protein_id="AA09644.1"
/db_xref="GI:1145330"
/translation="QVQLDQSGAEVKKPSQSLKISCKGSGYSTSYWIAVRQMPGK LEYMGILIPEDYTKYSPFSGQVTISVDKSVSTAYLQWSSLKPSDVAVFCAHDVG YCSSNCAKPEYFGHWGGTLTVSS"

ALIGNMENT SCORES:
Pred. No.: 5,77e-74 Length: 387
Score: 683.00 Matches: 126
Percent Similarity: 97.7% Conservative: 0
Best Local Similarity: 97.7% Mismatches: 3
Query Match: 97.6% Indels: 0
DB: 5 Gaps: 0

US-10-092-640-32 (1-129) x HSU8334 (1-387)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysPProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGACAGCTGTTGACGCTGGGGGAGAGTTGAAGAGCCGGGAGATCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
DB 61 TCCTGTAAGGGTTCGTGATACAGCTTACCACTGAGTCCCTGGGGCCGCAAGT 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
DB 121 CCGGGAAAGGCGCTGAGTACATGGGGCTCATCTATCTGGTATTAATGTTACCAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 AGCCGCTCTTCCAAAGCCAGTCAACCATCTCAGTCGACAAAGTCCGTCAGCATCGCTAC 240
QY 81 LeuGlnTyrSerSerLeuLysPProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTGCAATGAGCAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGGGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerSerSerValAlaValTyrProGlyLysPheGlnHisTrpGly 120
DB 301 GTGGGATATTGGAGATGATTCACACTGCGCAAGTGGCTGAATATCTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGTACCTGTGTACCCGTCTCTCA 387

RESULT 15
HSU36543 387 bp mRNA linear PRI 04-JAN-1996
LOCUS HSU36543
DEFINITION Human anti-c-erbB-2 immunoglobulin heavy chain V region mRNA,
partial cds.
ACCESSION U36543

VERSION U36543.1 GI:1145225
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 387)
AUTHORS Schier, R., Bye, J., Apell, G., McCall, A., Adams, G.P., Weiner, L.W. and Marks, J.D.
TITLE Isolation of high affinity monomeric Human anti-c-erbB-2 single chain Fv using affinity driven selection
JOURNAL J. Mol. Biol. (1995) In press
REFERENCE 2 (bases 1 to 387)
AUTHORS Schier, R.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1995) Robert Schier, Anesthesia, University of California at San Francisco, 1001 Potrero Avenue, San Francisco, CA 94110, USA
FEATURES
source location/Qualifiers
1..387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CGH1"
<1..387
/codon_start=1
/product="anti-c-erbB-2 immunoglobulin heavy chain v region"
/protein_id="AA05075.1"
/db_xref="GI:1145226"
/translation="QVQLVDSGAEVKKPSQSLKISCKGSGYSTSYWIAVRQMPGK LEYMGILIPGDSVTKYSPFSGQVTISVDKSVSTAYLQWSSLKPSDVAVFCAHDVG YCSSNCAKPEYFGHWGGTLTVSS"

ALIGNMENT SCORES:
Pred. No.: 7.66e-74 Length: 387
Score: 682.00 Matches: 123
Percent Similarity: 100.0% Conservative: 6
Best Local Similarity: 95.3% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 5 Gaps: 0

US-10-092-640-32 (1-129) x HSU36543 (1-387)

QY 1 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysPProGlyGlnSerLeuLysIle 20
DB 1 CAGGTGACAGCTGTTGACGCTGGGGGAGAGTTGAAGAGCCGGGAGATCTCGAAGATC 60
QY 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgIleMet 40
DB 61 TCCTGTAAGGGTTCGTGATACAGCTTACCACTGAGTCCCTGGGGCCGCAAGT 120
QY 41 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyLysPheSerAspThrLysTyr 60
DB 121 CCGGGAAAGGCGCTGAGTACATGGGGCTCATCTATCTGGTATTAATGTTACCAATAC 180
QY 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
DB 181 AGCCGCTCTTCCAAAGCCAGTCAACCATCTCAGTCGACAAAGTCCGTCAGCATCGCTAC 240
QY 81 LeuGlnTyrSerSerLeuLysPProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
DB 241 TTGCAATGAGCAGCTGTGAAGCCCTCGACAGCGCGGTGATTTTGTGGGAGACATGAC 300
QY 101 ValGlyTyrCysSerSerSerSerSerSerValAlaValTyrProGlyLysPheGlnHisTrpGly 120
DB 301 GTGGGATATTGGAGATGATTCACACTGCGCAAGTGGCTGAATATCTTCCAGCATTTGGGGC 360
QY 121 GlnGlyThrLeuValThrValSerSer 129
DB 361 CAGGGTACCTGTGTACCCGTCTCTCA 387

Fri May 26 08:42:21 2006

us-10-092-640-32.rge

Page 10

Search completed: May 25, 2006, 19:00:45
Job time : 4913.14 secs
